GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:23:06 ; Search time 611 Seconds
(without alignments)
7097.342 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5537552 seqs, 2974263231 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729	100.0	729	14	US-10-060-585-1	Sequence 1, Appli
2	729	100.0	729	18	US-10-334-235-1	Sequence 1, Appli
3	729	100.0	729	19	US-10-787-881A-1	Sequence 1, Appli
4	678	93.0	1807	14	US-10-060-585-2	Sequence 2, Appli
5	678	93.0	1807	18	US-10-334-235-2	Sequence 2, Appli
6	678	93.0	1807	19	US-10-787-881A-2	Sequence 2, Appli
7	675	92.6	1467	14	US-10-060-585-3	Sequence 3, Appli
8	675	92.6	1467	18	US-10-334-235-3	Sequence 3, Appli
9	675	92.6	1467	19	US-10-787-881A-3	Sequence 3, Appli
10	576	79.0	1518	14	US-10-104-522-5	Sequence 5, Appli
11	576	79.0	1518	14	US-10-060-585-5	Sequence 5, Appli
12	576	79.0	1518	18	US-10-334-235-5	Sequence 5, Appli
13	576	79.0	1518	19	US-10-787-881A-5	Sequence 5, Appli
14	569	78.1	9100	18	US-10-334-235-16	Sequence 16, Appl
15	551	75.6	2090	14	US-10-104-522-6	Sequence 6, Appli
16	551	75.6	2090	14	US-10-060-585-6	Sequence 6, Appli
17	551	75.6	2090	18	US-10-334-235-6	Sequence 6, Appli
18	551	75.6	2090	19	US-10-787-881A-6	Sequence 6, Appli
19	138	18.9	723	18	US-10-405-123-2	Sequence 2, Appli
20	62	8.5	318	14	US-10-252-978-3	Sequence 3, Appli
21	62	8.5	318	16	US-10-428-662-9	Sequence 9, Appli
22	59	8.1	714	8	US-08-940-544-4	Sequence 4, Appli
23	59	8.1	714	15	US-10-075-947A-2	Sequence 2, Appli
24	59	8.1	1173	15	US-10-075-947A-4	Sequence 4, Appli
25	56	7.7	351	16	US-10-094-097B-198	Sequence 198, App
26	52	7.1	372	13	US-10-007-790-1	Sequence 1, Appli
27	52	7.1	405	10	US-09-726-258-36	Sequence 36, Appl
28	52	7.1	408	18	US-10-768-193-9	Sequence 9, Appli
29	52	7.1	762	10	US-09-726-258-43	Sequence 43, Appl
30	52	7.1	910	14	US-10-104-522-1	Sequence 1, Appli
31	52	7.1	2239	14	US-10-104-522-2	Sequence 2, Appli
32	51	7.0	324	19	US-10-488-673-5	Sequence 5, Appli
33	51	7.0	324	19	US-10-879-994-105	Sequence 105, App
34	51	7.0	351	18	US-10-816-938-9	Sequence 9, Appli
35	51	7.0	729	19	US-10-879-994-9	Sequence 9, Appli
36	51	7.0	795	14	US-10-114-716A-47	Sequence 47, Appl
37	51	7.0	1809	14	US-10-104-522-3	Sequence 3, Appli
38	50	6.9	405	17	US-10-389-155-59	Sequence 59, Appl
39	50	6.9	405	17	US-10-389-417-59	Sequence 59, Appl
40	50	6.9	405	17	US-10-452-357-68	Sequence 68, Appl
41	50	6.9	426	9	US-09-772-120-7	Sequence 7, Appli
42	50	6.9	1135	10	US-09-203-958-2	Sequence 2, Appli
43	50	6.9	1314	9	US-09-903-327A-5	Sequence 5, Appli
44	50	6.9	1516	9	US-09-903-327A-1	Sequence 1, Appli
45	49	6.7	366	17	US-10-372-481-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYOU23.001CP1
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```
;   OTHER INFORMATION: 5T4 ScFv
US-10-060-585-1

  Query Match             100.0%;  Score 729;  DB 14;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 2
US-10-334-235-1
; Sequence 1, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding a 5T4 scFv, designated 5T4scFv.1
US-10-334-235-1

  Query Match             100.0%;  Score 729;  DB 18;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
```

```
                ||||||||
Db        721 ATCAAACGG 729


RESULT 3
US-10-787-881A-1
; Sequence 1, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
;  APPLICANT: Oxford BioMedica (UK) Ltd.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: Vector
;  FILE REFERENCE: 021911-000330US
;  CURRENT APPLICATION NUMBER: US/10/787,881A
;  CURRENT FILING DATE:  2004-02-25
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/01627
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Coding sequence of 5T4scFv
US-10-787-881A-1

  Query Match             100.0%;  Score 729;  DB 19;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 4
US-10-060-585-2
; Sequence 2, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
;  APPLICANT: Kingsman, Alan J.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 5T4Sab1
US-10-060-585-2

  Query Match             93.0%;  Score 678;  DB 14;  Length 1807;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308
```

```
Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 5
US-10-334-235-2
; Sequence 2, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxfard Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA sequence encoding 5T4Sabi
US-10-334-235-2

Query Match 93.0%; Score 678; DB 18; Length 1807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 6
US-10-787-881A-2
; Sequence 2, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford BioMedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627

```
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence encoding 5T4 single chain antibody
US-10-787-881A-2

  Query Match            93.0%;  Score 678;  DB 19;  Length 1807;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 7
US-10-060-585-3
; Sequence 3, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
;  APPLICANT: Kingsman, Alan J.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7-1.5T4.1
US-10-060-585-3

  Query Match            92.6%;  Score 675;  DB 14;  Length 1467;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
                ||||||
Db       1459 ATCAAA 1464
```

RESULT 8
US-10-334-235-3
; Sequence 3, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxfard Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of B7-1.5T4.1
US-10-334-235-3

Query Match 92.6%; Score 675; DB 18; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

RESULT 9
US-10-787-881A-3
; Sequence 3, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford BioMedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding fusion protein B7-1.5T4.1
US-10-787-881A-3

Query Match 92.6%; Score 675; DB 19; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858
```

```
Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

RESULT 10
US-10-104-522-5
; Sequence 5, Application US/10104522
; Publication No. US20030018004A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, C.R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: DYOU23.001DV1
; CURRENT APPLICATION NUMBER: US/10/104,522
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/445375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBSII/Leader/scFv/HG1.
US-10-104-522-5

Query Match 79.0%; Score 576; DB 14; Length 1518;
Best Local Similarity 99.6%; Pred. No. 6e-294;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 11
US-10-060-585-5
; Sequence 5, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.

```
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7 link ScFv sequence
US-10-060-585-5

  Query Match             79.0%;  Score 576;  DB 14;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 6e-294;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 12
US-10-334-235-5
; Sequence 5, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7 Link scFv sequence
US-10-334-235-5

  Query Match             79.0%;  Score 576;  DB 18;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 6e-294;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
```

```
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 13
US-10-787-881A-5
; Sequence 5, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford BioMedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence encoding B7 Link scFv
US-10-787-881A-5

Query Match 79.0%; Score 576; DB 19; Length 1518;
Best Local Similarity 99.6%; Pred. No. 6e-294;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 14
US-10-334-235-16
; Sequence 16, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 9100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nuc sequence of the SMART2 LscFvB7.1 5' cPPT
; OTHER INFORMATION: plasmid

US-10-334-235-16

Query Match 78.1%; Score 569; DB 18; Length 9100;
Best Local Similarity 99.6%; Pred. No. 2.9e-290;
Matches 719; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 3706

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 3766

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 3826

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 3886

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 3946

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       3947 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 4006

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4007 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 4066

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4067 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 4126

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       4127 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 4186

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4187 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 4246

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4247 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 4306

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4307 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 4366

Qy        721 AT 722
              ||
Db       4367 AT 4368
```

RESULT 15
US-10-104-522-6
; Sequence 6, Application US/10104522
; Publication No. US20030018004A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, C.R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: DYOU23.001DV1
; CURRENT APPLICATION NUMBER: US/10/104,522
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/445375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5T4 scFv-human IgE fusion construct.
US-10-104-522-6

Query Match 75.6%; Score 551; DB 14; Length 2090;
Best Local Similarity 99.6%; Pred. No. 1e-280;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 140

Qy         73 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 200

Qy        133 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 260

Qy        193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 320

Qy        253 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 380

Qy        313 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGG 372
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db        381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGG 440

Qy        373 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 500

Qy        433 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 560

Qy        493 AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 552
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        561 AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 620

Qy        553 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 680

Qy        613 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740

Qy        673 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 716
              |||||||||||||||||||||||||||||||||||||||||||||
Db        741 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 784
```

Search completed: March 16, 2005, 00:46:20

Job time : 615 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 20:38:45 ; Search time 3427 Seconds
(without alignments)
8097.126 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	117	16.0	842	9	BX969451	BX969451 Reverse s
	2	86	11.8	724	2	BF168514	BF168514 601775412
	3	86	11.8	769	2	BF168856	BF168856 601775314
	4	66	9.1	507	2	BF015548	BF015548 uy23a08.y
	5	61	8.4	594	2	BE309592	BE309592 601094848
	6	61	8.4	883	2	BF580610	BF580610 602093730
c	7	59	8.1	638	8	AZ706203	AZ706203 RPCI-23-2
	8	56	7.7	348	8	AZ611733	AZ611733 1M0438F15
	9	56	7.7	635	8	AZ610015	AZ610015 1M0435N01
	10	52	7.1	784	8	BH121432	BH121432 RPCI-24-3
	11	47	6.4	320	5	BY346210	BY346210 BY346210
	12	47	6.4	529	6	CA577954	CA577954 K0716F08-
	13	47	6.4	598	4	BI104341	BI104341 602889919
	14	47	6.4	607	1	AV259014	AV259014 AV259014
	15	47	6.4	640	5	BQ109114	BQ109114 imageqc_6
	16	47	6.4	754	9	CR026392	CR026392 Reverse s
	17	47	6.4	794	4	BI150371	BI150371 602915205
	18	47	6.4	801	5	BU946353	BU946353 AGENCOURT
	19	47	6.4	1576	3	AK007918	AK007918 Mus muscu
c	20	46	6.3	408	9	BX980485	BX980485 Forward s
	21	46	6.3	422	6	CA578211	CA578211 K0720E02-
	22	46	6.3	465	6	CA578116	CA578116 K0718G11-
	23	46	6.3	469	6	CA574907	CA574907 K0622H02-
	24	46	6.3	472	6	CA578323	CA578323 K0722B03-
	25	46	6.3	493	6	CA572170	CA572170 K0531B11-
	26	46	6.3	508	6	CA571278	CA571278 K0518B06-
	27	46	6.3	508	6	CA577080	CA577080 K0704C12-
	28	46	6.3	514	6	CA577707	CA577707 K0713C01-
	29	46	6.3	538	6	CA578968	CA578968 K0731A04-
	30	46	6.3	538	6	CA580316	CA580316 K0749H01-
	31	46	6.3	623	4	BG964955	BG964955 602829272
	32	46	6.3	639	2	BE371136	BE371136 601218628
	33	46	6.3	692	6	BY707828	BY707828 BY707828
	34	46	6.3	1010	5	BQ921928	BQ921928 AGENCOURT
	35	46	6.3	1524	3	AK007826	AK007826 Mus muscu
	36	45	6.2	480	8	AZ892554	AZ892554 RPCI-24-1
c	37	45	6.2	509	8	AZ791472	AZ791472 2M0041H23
	38	45	6.2	667	6	BY724790	BY724790 BY724790
	39	45	6.2	776	5	BU517736	BU517736 AGENCOURT
	40	44	6.0	350	6	BY794132	BY794132 BY794132
	41	44	6.0	356	5	BY117980	BY117980 BY117980
	42	44	6.0	360	5	BY119951	BY119951 BY119951
	43	44	6.0	501	6	CA577443	CA577443 K0709F01-
	44	44	6.0	501	6	CA579132	CA579132 K0733B12-
	45	44	6.0	501	6	CA579461	CA579461 K0737G06-

ALIGNMENTS

RESULT 1
BX969451
LOCUS BX969451 842 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN79o16, genomic survey sequence.
ACCESSION BX969451
VERSION BX969451.1 GI:49700874
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 842)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES Location/Qualifiers
source 1. .842
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN79o16"
/clone_lib="MHPN"
ORIGIN

Query Match 16.0%; Score 117; DB 9; Length 842;
Best Local Similarity 100.0%; Pred. No. 4.7e-51;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 373

Qy         91 GGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGA 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGA 430
```

RESULT 2
BF168514
LOCUS BF168514 724 bp mRNA linear EST 30-OCT-2000
DEFINITION 601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5', mRNA sequence.
ACCESSION BF168514

```
VERSION     BF168514.1  GI:11048866
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9265  row: h  column: 04
            High quality sequence stop: 661.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4017075"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             11.8%;  Score 86;  DB 2;  Length 724;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-34;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 184

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
              ||||||||||||||||||||||||||
Db        185 GGCTACTACATGCACTGGGTGAAGCA 210


RESULT 3
BF168856
LOCUS       BF168856                769 bp    mRNA    linear   EST 30-OCT-2000
DEFINITION  601775314F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017147 5',
            mRNA sequence.
ACCESSION   BF168856
VERSION     BF168856.1  GI:11049208
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9265  row: k  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .769
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4017147"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             11.8%;  Score 86;  DB 2;  Length 769;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-34;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 188

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
              ||||||||||||||||||||||||||
Db        189 GGCTACTACATGCACTGGGTGAAGCA 214


RESULT 4
BF015548
LOCUS       BF015548                507 bp    mRNA    linear   EST 29-DEC-2000
DEFINITION  uy23a08.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3660374 5'
            similar to SW:HV14_MOUSE P01758 IG HEAVY CHAIN V REGION 108A
            PRECURSOR. ;, mRNA sequence.
ACCESSION   BF015548
VERSION     BF015548.1  GI:10746880
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

            MGI:1421142
            Seq primer: -40RP from Gibco
            High quality sequence stop: 456.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3660374"
```

```
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu30"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: Oligo
                     dT.   Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             9.1%;  Score 66;  DB 2;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         83 CATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGA 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 CATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGA 233

Qy        143 TTGGAC 148
              ||||||
Db        234 TTGGAC 239


RESULT 5
BE309592
LOCUS       BE309592                 594 bp    mRNA    linear   EST 26-OCT-2000
DEFINITION  601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
            mRNA sequence.
ACCESSION   BE309592
VERSION     BE309592.1  GI:9168025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8530  row: o  column: 12
            High quality sequence stop: 591.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="mix FVB/N, C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3489635"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam5"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
ORIGIN

  Query Match             8.4%;  Score 61;  DB 2;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 6e-21;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        445 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA 145

Qy        505 G 505
              |
Db        146 G 146


RESULT 6
BF580610
LOCUS       BF580610                 883 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5',
            mRNA sequence.
ACCESSION   BF580610
VERSION     BF580610.1  GI:11654322
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9771  row: l  column: 07
            High quality sequence stop: 639.
FEATURES             Location/Qualifiers
     source          1. .883
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4208022"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             8.4%;  Score 61;  DB 2;  Length 883;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-21;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        445 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA 169

Qy        505 G 505
              |
Db        170 G 170


RESULT 7
AZ706203/c
LOCUS       AZ706203                 638 bp    DNA     linear   GSS 24-JAN-2001
DEFINITION  RPCI-23-236G24.TJ RPCI-23 Mus musculus genomic clone
            RPCI-23-236G24, genomic survey sequence.
ACCESSION   AZ706203
VERSION     AZ706203.1  GI:12433429
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
```

```
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-236G24.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 236  row: G  column: 24
            Seq primer: SP6
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .638
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="RPCI-23-236G24"
                      /sex="Female"
                      /lab_host="DH10B"
                      /clone_lib="RPCI-23"
                      /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                      EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                      brain genomic DNA was isolated and  partially digested
                      with a combination of EcoRI and EcoRI Methylase.   Size
                      selected DNA was cloned into the pBACe3.6 vector at the
                      EcoRI  sites.  The ligation products were transformed into
                      DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             8.1%;  Score 59;  DB 8;  Length 638;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-20;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 AGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAG 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 AGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAG 544


RESULT 8
AZ611733
LOCUS       AZ611733                348 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0438F15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0438F15 F, genomic survey sequence.
ACCESSION   AZ611733
VERSION     AZ611733.1  GI:11733923
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0438  row: F  column: 15
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 348.
FEATURES              Location/Qualifiers
     source           1. .348
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0438F15"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             7.7%;  Score 56;  DB 8;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 332


RESULT 9
AZ610015
LOCUS       AZ610015                635 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0435N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0435N01 F, genomic survey sequence.
ACCESSION   AZ610015
VERSION     AZ610015.1  GI:11732205
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
```

```
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0435  row: N  column: 01
          Seq primer: CGTTGTAAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 635.
FEATURES             Location/Qualifiers
     source          1. .635
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0435N01"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             7.7%;  Score 56;  DB 8;  Length 635;
  Best Local Similarity   100.0%;  Pred. No. 3e-18;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 363


RESULT 10
BH121432
LOCUS       BH121432                 784 bp    DNA     linear   GSS 19-JUL-2001
DEFINITION  RPCI-24-300D2.TV RPCI-24 Mus musculus genomic clone RPCI-24-300D2,
            genomic survey sequence.
ACCESSION   BH121432
VERSION     BH121432.1  GI:14964944
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-24-300D2.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 300  row: D  column: 2
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .784
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-300D2"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
ORIGIN

  Query Match             7.1%;  Score 52;  DB 8;  Length 784;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-16;
  Matches   52;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         97 TACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 TACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 503


RESULT 11
BY346210
LOCUS       BY346210                 320 bp    mRNA    linear   EST 12-DEC-2002
DEFINITION  BY346210 RIKEN full-length enriched, whole joints Mus musculus cDNA
            clone L730022G23 5', mRNA sequence.
ACCESSION   BY346210
VERSION     BY346210.1  GI:26575698
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 320)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
```

```
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
  MEDLINE   22354683
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
            Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
            Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
            Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
            Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
            Hayashizaki,Y. Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
            Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
            Fleming street 16672 Vari,Greece ) whose assistance we gratefully
            acknowledge.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .320
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="L730022G23"
                     /tissue_type="whole joints"
                     /clone_lib="RIKEN full-length enriched, whole joints"
ORIGIN

  Query Match             6.4%;  Score 47;  DB 5;  Length 320;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
              |||||||||||||||||||||||||||||||||||||||||||||
Db        135 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 181


RESULT 12
CA577954
LOCUS       CA577954                529 bp    mRNA    linear   EST 19-NOV-2002
DEFINITION  K0716F08-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
            cDNA Library (Long) Mus musculus cDNA clone NIA:K0716F08
            IMAGE:30075139 5', mRNA sequence.
ACCESSION   CA577954
VERSION     CA577954.1  GI:25126345
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G.,
            Aiba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
  TITLE     Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
            (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: K0716F08-3
            Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: K0716  row: F  column: 08
            Seq primer: M13 Reverse
            High quality sequence stop: 529
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .529
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6NCr"
                     /db_xref="niaEST:K0716F08-5N"
                     /db_xref="taxon:10090"
                     /clone="NIA:K0716F08 IMAGE:30075139"
                     /tissue_type="Hematopoietic Stem Cell
                     (Lin-/c-Kit-/Sca-1-)"
                     /dev_stage="Age approx.10 weeks old"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Hematopoietic Stem Cell
                     (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
                     /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
                     NotI; Mouse cDNA project by the Laboratory of Genetics,
                     National Institute on Aging (NIA), Intramural Research
                     Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
                     a long-transcript enriched cDNA library (Ref. Genome Res.
                     11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
                     obtained from Drs. Dennis Taub, Dan Longo (National
                     Institute on Aging, USA), Jonathan Keller (National Cancer
                     Institute, USA). Double-stranded cDNAs were synthesized
                     with an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     0.9 ug of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pSPORT1 plasmid vector.
                     The DH10B E. coli host was transformed with the ligation
                     mixture by the standard chemical method. The average
                     insert size is about 2.1 kb. The library was constructed
                     by Yulan Piao (NIA)."
ORIGIN

  Query Match             6.4%;  Score 47;  DB 6;  Length 529;
  Best Local Similarity   100.0%;  Pred. No. 2e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
              |||||||||||||||||||||||||||||||||||||||||||||
Db        110 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 156


RESULT 13
BI104341
```

```
LOCUS       BI104341                598 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602889919F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035013 5',
            mRNA sequence.
ACCESSION   BI104341
VERSION     BI104341.1  GI:14555234
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11097  row: f  column: 06
            High quality sequence stop: 598.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5035013"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             6.4%;  Score 47;  DB 4;  Length 598;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
              |||||||||||||||||||||||||||||||||||||||||||||
Db        122 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 168


RESULT 14
AV259014
LOCUS       AV259014                607 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  AV259014 RIKEN full-length enriched, adult male testis (DH10B) Mus
            musculus cDNA clone 4930402P15 3' similar to M13787 Mouse Ig
            unrearranged transcribed H-chain V-region VH558 mRNA, clone A1/A4,
            mRNA sequence.
ACCESSION   AV259014
VERSION     AV259014.2  GI:16388564
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 607)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On Nov 4, 1999 this sequence version replaced gi:6246473.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .607
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="4930402P15"
                     /sex="male"
                     /tissue_type="testis"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male testis
                     (DH10B)"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

  Query Match             6.4%;  Score 47;  DB 1;  Length 607;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
```

```
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 183


RESULT 15
BQ109114
LOCUS       BQ109114                640 bp    mRNA    linear   EST 16-APR-2002
DEFINITION  imageqc_6_2001/snl21bdrr81.y1 NCI_CGAP_Lu29 Mus musculus cDNA clone
            IMAGE:5035013 5', mRNA sequence.
ACCESSION   BQ109114
VERSION     BQ109114.1  GI:20158768
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
            Prange,C.K.
  TITLE     The I.M.A.G.E. Consortium quality control effort: clone
            resequencing for verification
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: BI104341
            Contact: Prange CK
            The I.M.A.G.E. Consortium
            Lawrence Livermore National Laboratory
            Livermore, CA, USA
            Email: help@image.llnl.gov
            This read has been verified (found to hit its original self in the
            correct orientation), as part of the I.M.A.G.E. Consortium quality
            control effort. High quality sequence is defined as having 100 or
            more base pairs with a phred quality value of 20 or greater, where
            a sliding window of 4 base pairs with a phred quality value of 15
            or greater marks the beginning and end of the sequence. For
            information on obtaining this clone, please contact
            info@image.llnl.gov.
            Plate: LLAM11097  row: f  column: 6
            Seq primer: m13rp1
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5035013"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             6.4%;  Score 47;  DB 5;  Length 640;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 168


Search completed: March 15, 2005, 23:20:20
Job time : 3434 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 18:05:05 ; Search time 3818 Seconds
(without alignments)
9251.926 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729	100.0	729	6	BD136150	BD136150 Vector. 9
2	729	100.0	729	6	AX002778	AX002778 Sequence
3	729	100.0	729	6	AX149544	AX149544 Sequence
4	678	93.0	729	6	BD136268	BD136268 Enhanceme
5	678	93.0	729	6	AX018532	AX018532 Sequence
6	678	93.0	729	6	AX018608	AX018608 Sequence
7	678	93.0	1807	6	BD136151	BD136151 Vector. 9
8	678	93.0	1807	6	AX002779	AX002779 Sequence
9	675	92.6	1467	6	BD136152	BD136152 Vector. 9
10	675	92.6	1467	6	AX002780	AX002780 Sequence
11	675	92.6	1467	6	AX149546	AX149546 Sequence
12	576	79.0	1518	6	BD136154	BD136154 Vector. 9
13	576	79.0	1518	6	AX002782	AX002782 Sequence
14	576	79.0	1518	6	AX149550	AX149550 Sequence
15	551	75.6	1796	6	AX149547	AX149547 Sequence
16	551	75.6	2090	6	BD136155	BD136155 Vector. 9
17	551	75.6	2090	6	AX002783	AX002783 Sequence
18	551	75.6	2090	6	AX149551	AX149551 Sequence
19	126	17.3	330	10	AY369876	AY369876 Mus muscu
20	126	17.3	342	10	AF083186	AF083186 Mus muscu
21	101	13.9	548	10	MUSIGHVBB	D13201 Mus musculu
22	101	13.9	653	10	MMIGVH9	X02462 Mouse germl
23	98	13.4	130805	2	AC116524	AC116524 Mus muscu
24	98	13.4	180673	10	AC073565	AC073565 Mus muscu
25	86	11.8	294	10	AF303833	AF303833 Mus muscu
26	86	11.8	321	10	AY172007	AY172007 Mus muscu
27	86	11.8	354	10	MMU60461	U60461 Mus musculu
28	86	11.8	370	10	AY436962	AY436962 Mus muscu
29	86	11.8	375	10	AY436970	AY436970 Mus muscu
30	86	11.8	384	10	AY639151	AY639151 Mus muscu
31	86	11.8	387	10	AF276290	AF276290 Mus muscu
32	86	11.8	729	6	AR027053	AR027053 Sequence
33	86	11.8	729	6	E10362	E10362 cDNA encodi
34	86	11.8	729	6	I31036	I31036 Sequence 3
35	86	11.8	209058	10	AC079181	AC079181 Mus muscu
c 36	84	11.5	202704	10	AC090843	AC090843 Mus muscu
37	81	11.1	324	10	MUSIKCVRJ	D50385 Mus musculu
38	80	11.0	735	12	AF162710	AF162710 Synthetic
39	77	10.6	323	10	MMIGHT82	X59206 Mouse immun
40	74	10.2	363	10	MUSAI	L48677 Mus musculu
41	74	10.2	435	10	MMMABAB	X67191 M.musculus
42	74	10.2	475	10	MMMABAA	X67190 M.musculus
43	72	9.9	333	10	MMU88668	U88668 Mus musculu
44	72	9.9	336	10	AY089724	AY089724 Mus muscu
45	72	9.9	345	10	MMU88677	U88677 Mus musculu

ALIGNMENTS

RESULT 1
BD136150
LOCUS BD136150 729 bp DNA linear PAT 18-SEP-2002
DEFINITION Vector.
ACCESSION BD136150
VERSION BD136150.1 GI:23231095
KEYWORDS JP 2002507117-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 729)
AUTHORS Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and Myers,K.A.
TITLE Vector
JOURNAL Patent: JP 2002507117-A 1 05-MAR-2002;
OXFORD BIOMEDICA LTD
COMMENT OS Artificial Sequence
PN JP 2002507117-A/1
PD 05-MAR-2002
PF 04-JUN-1998 JP 1999501858
PR 04-JUN-1997 GB 9711579.4,20-JUN-1997 GB 9713150.2 PR 04-JUL-1997 GB 9714230.1
PI SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA PI MARGARET ELLARD,
PI MILES WILLIAM CARROLL,KEVIN ALAN MYERS
PC C12N15/85,A61K48/00
CC Description of Artificial Sequence: DNA
FH Key Location/Qualifiers
FT source 1. .729
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 729; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

```
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
Db        721 ATCAAACGG 729
```

```
RESULT 2
AX002778
LOCUS       AX002778                729 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9855607.
ACCESSION   AX002778
VERSION     AX002778.1  GI:9885103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 1 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             <1. .>729
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04191.1"
                     /db_xref="GI:9885104"
                     /translation="EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKS
                     LEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI
                     TNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKA
                     SQSVSNDVXWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDL
                     AVYFCQQDYNSPPTFGGGTKLEIKR"
ORIGIN

  Query Match           100.0%;  Score 729;  DB 6;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
Db        721 ATCAAACGG 729
```

RESULT 3

```
AX149544
LOCUS       AX149544                729 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 5 from Patent WO0136486.
ACCESSION   AX149544
VERSION     AX149544.1  GI:14347983
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 5 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5T4ScFv.1"
ORIGIN

  Query Match           100.0%;  Score 729;  DB 6;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 4
BD136268
LOCUS       BD136268                729 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Enhancement of prodrug activation.
ACCESSION   BD136268
VERSION     BD136268.1  GI:23231213
KEYWORDS    JP 2002505341-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 729)
  AUTHORS   Stratford,I.J., Patterson,A.V., Kingsman,S.M., Kan,O., Griffiths,L.
            and Mitrophanous,K.
  TITLE     Enhancement of prodrug activation
  JOURNAL   Patent: JP 2002505341-A 21 19-FEB-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002505341-A/21
            PD   19-FEB-2002
            PF   05-MAR-1999 JP 2000534657
            PR   06-MAR-1998 GB    9804841.6,19-AUG-1998 GB    9818103.5 PR
            29-JAN-1999 GB    9902081.0
            PI   IAN JAMES STRATFORD,ADAM VORN PATTERSON,SUSAN MARY KINGSMAN,ON

            PI   KAN,
            PI   LEIGH GRIFFITHS,KYRIACOS MITROPHANOUS
            PC   A61K47/48,A61K35/76,A61K38/44,A61K45/00,A61K48/00,A61P9/10, PC
              A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N7/00,C12N9/02,C12N15/09, PC
            A61K37/50,
            PC   C12N5/00,C12N15/00
            CC   Description of Artificial Sequence: Synthetic sequence FH
            Key             Location/Qualifiers
            FT   source          1. .729
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           93.0%;  Score 678;  DB 6;  Length 729;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
```

```
Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 5
AX018532
LOCUS AX018532 729 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent WO9945127.
ACCESSION AX018532
VERSION AX018532.1 GI:10042675
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J., Griffiths,L. and Kan,O.
TITLE Enhanced prodrug activation
JOURNAL Patent: WO 9945127-A 26 10-SEP-1999;
KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN ON (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 93.0%; Score 678; DB 6; Length 729;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 6
AX018608
LOCUS AX018608 729 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent WO9945126.
ACCESSION AX018608
VERSION AX018608.1 GI:10042738
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J., Griffiths,L. and Kan,O.
TITLE Enhanced prodrug activation
JOURNAL Patent: WO 9945126-A 26 10-SEP-1999;
KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN ON (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 93.0%; Score 678; DB 6; Length 729;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

```
RESULT 7
BD136151
LOCUS       BD136151                1807 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136151
VERSION     BD136151.1  GI:23231096
KEYWORDS    JP 2002507117-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1807)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 2 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/2
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: cDNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1807
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1807
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             93.0%;  Score 678;  DB 6;  Length 1807;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797

RESULT 8
```

```
AX002779
LOCUS       AX002779               1807 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9855607.
ACCESSION   AX002779
VERSION     AX002779.1  GI:9885105
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 2 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1807
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             <3. .1790
                     /note="unnamed protein product; cDNA"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04205.1"
                     /db_xref="GI:9885106"
                     /translation="ASTMGWSCIILFLVATATGVHSEVQLQQSGPDLVKPGASVKISC
                     KASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAY
                     MELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIV
                     MTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDR
                     FIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLEIKRASTKGPSVFPL
                     APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
                     TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
                     PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
                     VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                     NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                     QGNVFSCSVMHEALHNHYTQKSLSLSPGK"
ORIGIN

  Query Match           93.0%;  Score 678;  DB 6;  Length 1807;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 9
BD136152
LOCUS       BD136152               1467 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136152
VERSION     BD136152.1  GI:23231097
KEYWORDS    JP 2002507117-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1467)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 3 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/3
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1467
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           92.6%;  Score 675;  DB 6;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858
```

```
Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

```
RESULT 10
AX002780
LOCUS       AX002780               1467 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 3 from Patent WO9855607.
ACCESSION   AX002780
VERSION     AX002780.1  GI:9885107
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 3 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             1. .1467
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04192.1"
                     /db_xref="GI:9885108"
                     /translation="MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKE
                     VATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIV
                     ILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
                     ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLI
                     KYGHLRVNQTFNWNTTKQEHFPDGGGGSEVQLQQSGPDLVKPGASVKISCKASGYSFT
                     GYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAYMELRSLTS
                     EDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIVMTQTPTFL
                     LVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGT
                     DFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLEIK"
ORIGIN
```

```
  Query Match             92.6%;  Score 675;  DB 6;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

```
RESULT 11
AX149546
LOCUS       AX149546               1467 bp    DNA     linear   PAT 08-JUN-2001
```

```
DEFINITION  Sequence 7 from Patent WO0136486.
ACCESSION   AX149546
VERSION     AX149546.1  GI:14347985
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 7 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="B7-1.5T4ScFv.1"
ORIGIN

  Query Match           92.6%;  Score 675;  DB 6;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464


RESULT 12
BD136154
LOCUS       BD136154                1518 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136154
VERSION     BD136154.1  GI:23231099
KEYWORDS    JP 2002507117-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1518)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 5 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/5
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1518
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           79.0%;  Score 576;  DB 6;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206
```

```
Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 13
AX002782
LOCUS       AX002782               1518 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9855607.
ACCESSION   AX002782
VERSION     AX002782.1  GI:9885111
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 5 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA"
ORIGIN

  Query Match             79.0%;  Score 576;  DB 6;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 14
AX149550
LOCUS       AX149550               1518 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 11 from Patent WO0136486.
ACCESSION   AX149550
VERSION     AX149550.1  GI:14347988
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 11 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="B7-ScFv"
ORIGIN

  Query Match             79.0%;  Score 576;  DB 6;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
```

```
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729

Db       1507 ATCAAACGG 1515
```

```
RESULT 15
AX149547
LOCUS       AX149547               1796 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 8 from Patent WO0136486.
ACCESSION   AX149547
VERSION     AX149547.1  GI:14347986
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 8 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1796
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5T4ScFv.1-IgG"
ORIGIN
```

```
  Query Match           75.6%;  Score 551;  DB 6;  Length 1796;
  Best Local Similarity   99.6%;  Pred. No. 4.3e-305;
  Matches  701;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 72

Db         81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 140

Qy         73 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132

Db        141 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 200

Qy        133 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 192

Db        201 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 260

Qy        193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 252

Db        261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 320

Qy        253 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 312

Db        321 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 380

Qy        313 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGG 372

Db        381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGG 440

Qy        373 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 432

Db        441 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 500

Qy        433 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 492

Db        501 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 560

Qy        493 AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 552

Db        561 AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 620

Qy        553 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 612

Db        621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 680

Qy        613 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 672

Db        681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740

Qy        673 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 716

Db        741 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 784
```

```
Search completed: March 15, 2005, 22:23:03
Job time : 3824 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 16:13:19 ; Search time 584 Seconds
(without alignments)
7389.540 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729	100.0	729	2	AAV80290	Aav80290 Murine an
2	729	100.0	729	4	AAF89729	Aaf89729 Nucleotid
3	678	93.0	729	2	AAZ19786	Aaz19786 Anti-5T4
4	678	93.0	729	2	AAZ07810	Aaz07810 5T4 scFv
5	678	93.0	1807	2	AAV80291	Aav80291 Anti-5T4
6	675	92.6	1467	2	AAV80292	Aav80292 Human B7-
7	675	92.6	1467	4	AAF89730	Aaf89730 Nucleotid
8	576	79.0	1518	2	AAV80294	Aav80294 B7-1/scFv
9	576	79.0	1518	4	AAF89732	Aaf89732 Nucleotid
10	551	75.6	1796	4	AAF89733	Aaf89733 Nucleotid
11	551	75.6	2090	2	AAV80295	Aav80295 ScFv-IgE1
12	551	75.6	2090	4	AAF89734	Aaf89734 Nucleotid
13	86	11.8	729	2	AAQ73679	Aaq73679 Fv(GP-4)
14	86	11.8	1413	12	ADM72026	Adm72026 Chimeric
15	66	9.1	334	2	AAT43737	Aat43737 Anti-DNA
16	66	9.1	1401	9	AAD58178	Aad58178 Mouse vir
17	63	8.6	906	2	AAV00611	Aav00611 Anti-huma
18	62	8.5	318	2	AAQ46080	Aaq46080 Sequence
19	62	8.5	318	2	AAQ47059	Aaq47059 HP1/2 Vk.
20	62	8.5	318	2	AAQ67344	Aaq67344 Anti-VLA4
21	62	8.5	318	2	AAQ65623	Aaq65623 HP1/2 lig
22	62	8.5	318	2	AAQ69193	Aaq69193 HP1/2 Vk
23	62	8.5	318	2	AAQ83571	Aaq83571 Anti-VLA-
24	62	8.5	318	2	AAV66800	Aav66800 Anti-VLA-
25	62	8.5	318	2	AAV02232	Aav02232 Anti-VLA-
26	62	8.5	318	2	AAX15094	Aax15094 cDNA enco
27	62	8.5	318	2	AAX27914	Aax27914 Anti VLA-
28	62	8.5	318	2	AAX86185	Aax86185 cDNA enco
29	62	8.5	318	4	AAF86602	Aaf86602 Murine an
30	62	8.5	318	8	ABX93815	Abx93815 Mouse ant
31	62	8.5	318	9	ACD28356	Acd28356 cDNA enco
32	62	8.5	318	10	ADI25184	Adi25184 Murine HP
33	62	8.5	318	12	ADF94348	Adf94348 Mouse ant
34	62	8.5	318	13	ADR40361	Adr40361 Anti-VLA-
35	62	8.5	318	13	ADR40279	Adr40279 Anti-VLA-
36	61	8.4	384	6	AAD46727	Aad46727 Chimeric
37	61	8.4	726	4	AAF30723	Aaf30723 Anti-FIX/
38	61	8.4	882	2	AAQ48038	Aaq48038 Monoclona
39	59	8.1	714	2	AAT86310	Aat86310 Single ch
40	59	8.1	714	6	ABA92027	Aba92027 Anti-disi
41	59	8.1	1173	2	AAT86312	Aat86312 Single ch
42	56	7.7	356	2	AAQ28522	Aaq28522 Hypercalc
43	56	7.7	357	10	ABT15845	Abt15845 Anti-huma
44	56	7.7	405	2	AAQ30754	Aaq30754 p12-h2. 3
45	56	7.7	828	10	ABT15854	Abt15854 Anti-huma

ALIGNMENTS

RESULT 1
AAV80290
ID AAV80290 standard; cDNA; 729 BP.
XX
AC AAV80290;
XX
DT 15-MAR-1999 (first entry)
XX
DE Murine anti-5T4 antigen monoclonal antibody scFv DNA.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; ss.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86002.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1A; 82pp; English.
XX
CC This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see
CC AAW86002), comprising the heavy chain variable region (VH) from the
CC murine 5T4 monoclonal antibody followed by a 15-amino acid flexible

```
CC   linker and the light chain variable region (VL) of the mouse 5T4
CC   antibody. The trophoblast cell surface antigen defined by monoclonal
CC   antibody 5T4 is expressed at high levels on the cells of a wide variety
CC   of human tumours. The 5T4scFv.1 DNA sequence can be used to construct
CC   single-chain antibodies (see AAV80291) and scFv fusion constructs (see
CC   AAV80292-96). The invention relates to a vector comprising a nucleotide
CC   sequence coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI) which encodes a protein of interest
CC   (POI), the vector being capable of delivering the NOI and/or POI to the
CC   tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC   vector is used to treat cancer, and may also used as a gene delivery
CC   system for introducing at least 1 gene encoding a TIP (preferably a
CC   tumour binding protein) into a haematopoietic cell lineage
XX
SQ   Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 729;  DB 2;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

```
RESULT 2
AAF89729
ID   AAF89729 standard; DNA; 729 BP.
XX
AC   AAF89729;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a 5T4 ScFv designated 5T4ScFv.1.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .729
FT                   /*tag=  a
FT                   /transl_except= (pos: 505. .507, aa: Ala)
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   P-PSDB; AAB83835.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Claim 7; Fig 1; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a 5T4 ScFv of the invention. The antibody comprises the VH and VL
CC   regions from murine 5T4 monoclonal antibody, joined by a linker sequence
XX
SQ   Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 729;  DB 4;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
```

```
Qy          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy         361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy         421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy         481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy         541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy         601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy         661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy         721 ATCAAACGG 729
               |||||||||
Db         721 ATCAAACGG 729
```

```
RESULT 3
AAZ19786
ID   AAZ19786 standard; DNA; 729 BP.
XX
AC   AAZ19786;
XX
DT   06-DEC-1999  (first entry)
XX
DE   Anti-5T4 secreted single chain antibody Fv fragment DNA.
XX
KW   Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
KW   nucleus; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .729
FT                   /*tag=  a
FT                   /product= "Anti-5T4 secreted single chain antibody Fv
FT                   fragment"
XX
PN   WO9945127-A2.
XX
PD   10-SEP-1999.
XX
PF   05-MAR-1999;   99WO-GB000674.
XX
PR   06-MAR-1998;   98GB-00004841.
PR   19-AUG-1998;   98GB-00018103.
PR   29-JAN-1999;   99GB-00002081.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Stratford IJ,  Patterson AV,  Kingsman SM,  Kan O,  Griffiths L;
PI   Mitrophanous K;
XX
DR   WPI; 1999-551046/46.
DR   P-PSDB; AAY42294.
XX
PT   New prodrug activating agent targeted to selected cells or tissues,
PT   particularly hypoxic cells, for treating e.g. tumors.
XX
PS   Example 9; Fig 3; 187pp; English.
XX
CC   This sequence represents an example of a DNA encoding a secreted single
CC   chain antibody Fv fragment, which is involved in transcellular
CC   localisation. In this example, the antibody is directed against the 5T4
CC   antigen. A secreted single chain antibody Fv fragment can be fused to
CC   cytochrome P450 reductase (P450R) derivatives such as anchorless P450R
CC   (AAY42287) or FN fragment (AAY42288). This enables the fusion protein to
CC   be delivered to other cells where it is then transported to the nucleus.
CC   Many drugs' sites of action are in the nucleus, rather than the
CC   cytoplasm, where P450R normally functions. P450R or its derivatives can
CC   be used to activate prodrugs to their active form via reduction.
CC   Administration of a prodrug is useful where the active drug may be
CC   metabolised before it reaches its site of action or where the active drug
CC   is cytotoxic, e.g., anticancer drugs. Targetted delivery of such prodrug
CC   activators allows a reduction in dose of the prodrug, and thus of
CC   systemic side-effects. P450R derivative fusion proteins, or vectors that
CC   express them, are specifically used to treat tumours, inflammation,
CC   atherosclerosis and muscular dystrophy, but may also be used to treat
CC   many other conditions, e.g., cerebral malaria, rheumatoid arthritis, or
CC   conditions associated with hypoxia, ischaemia or hypoglycemia, or to
CC   deliver antibiotics, antiviral agents, analgesics, anaesthetics, anti-
CC   inflammatories, antineoplastic agents and diagnostic agents
XX
SQ   Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;
```

```
  Query Match             93.0%;  Score 678;  DB 2;  Length 729;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
```

```
Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 4
AAZ07810
ID AAZ07810 standard; DNA; 729 BP.
XX
AC AAZ07810;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody encoding DNA.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
KW 5T4 scFv; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .729
FT /*tag= a
XX
PN WO9945126-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB000672.
XX
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
DR P-PSDB; AAY27407.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
XX
PS Example 9; Fig 3F; 149pp; English.
XX
CC The invention provides a new prodrug activating agent that comprises: (i)
CC a localization domain (LD; other than a tumor-selective antibody) and a
CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (iii) a modified hematopoietic
CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (ii). The prodrug activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of prodrug, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively in
CC hypoxic cells. The present sequence represents the DNA encoding the
CC single chain variable antibody fragment against the tumor antigen 5T4
CC (5T4 scFv). 5T4 scFv is used in the construction of a fusion protein
CC comprising 5T4 scFv and a human P450 reductase derivative alP450R
XX
SQ Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;

Query Match 93.0%; Score 678; DB 2; Length 729;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
```

```
Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 5
AAV80291
ID AAV80291 standard; cDNA; 1807 BP.
XX
AC AAV80291;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-5T4 single chain antibody 5T4Sab1 DNA.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sab1; ss.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 3. .1790
FT /*tag= a
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86003.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1B; 82pp; English.
XX
CC This DNA sequence encodes a single chain antibody (Sab), termed 5T4Sab1
CC (see AAW86003), comprising an scFv derived from murine monoclonal
CC antibody 5T4 (see AAW86002) and the human g1 constant region. It was
CC constructed from cassettes comprising a translation initiation signal and
CC signal peptide (see AAV80297), the sequence of the secreted portion of
CC 5T4scFv.1, and the sequence of the human g1 constant region genomic
CC clone. The trophoblast cell surface antigen defined by 5T4 is expressed
CC at high levels on the cells of a wide variety of human tumours. The
CC invention relates to a vector comprising a nucleotide sequence coding for
CC a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC of interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC treat cancer, and may also used as a gene delivery system for introducing
CC at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage
XX
SQ Sequence 1807 BP; 432 A; 543 C; 469 G; 363 T; 0 U; 0 Other;

```
  Query Match            93.0%;  Score 678;  DB 2;  Length 1807;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 6
AAV80292
ID AAV80292 standard; cDNA; 1467 BP.
XX
AC AAV80292;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human B7-1.5T4.1 gene fusion, specific for human 5T4.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; human; B7-1;
KW co-stimulatory molecule; ss.
XX
OS Mus sp.
OS Homo sapiens.

OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86004.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 5; Fig 2; 82pp; English.
XX
CC This DNA sequence encodes B7-1.5T4.1 (see AAW86004), a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human co-
CC stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. The cDNA can
CC be inserted into vector pCI to allow expression of the fusion protein in
CC mammalian cells. The trophoblast cell surface antigen defined by 5T4 is
CC expressed at high levels on the cells of a wide variety of human tumours.
CC The invention relates to a vector comprising a nucleotide sequence coding
CC for a tumour interacting protein (TIP) and optionally a nucleotide
CC sequence of interest (NOI) which encodes a protein of interest (POI), the
CC vector being capable of delivering the NOI and/or POI to the tumour
CC recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is
CC used to treat cancer, and may also used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour binding
CC protein) into a haematopoietic cell lineage. B7-1 is expected to bind
CC specifically to CD28 and CTLA-4 present on human T-cells
XX
SQ Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;

Query Match 92.6%; Score 675; DB 2; Length 1467;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

RESULT 7
AAF89730
ID AAF89730 standard; DNA; 1467 BP.
XX
AC AAF89730;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a B7-1.5T4.1 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1467
FT /*tag= a
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR P-PSDB; AAB83836.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a

```
PT   disease condition associated with disease associated molecule.
XX
PS   Claim 8; Fig 2; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a B7-1.5T4.1 fusion protein. This comprises the N-terminus of the
CC   5T4 ScFv is fused after amino acid 215 of human B7-1
XX
SQ   Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;

  Query Match             92.6%;  Score 675;  DB 4;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464


RESULT 8
AAV80294
ID   AAV80294 standard; cDNA; 1518 BP.
XX
AC   AAV80294;
XX
DT   17-OCT-2003  (revised)
DT   15-MAR-1999  (first entry)
XX
DE   B7-1/scFv specific for use in cancer gene therapy.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; scFv; mouse; B7-1;
KW   co-stimulatory molecule; ss.
XX
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 10; Page 63-64; 82pp; English.
XX
CC   This DNA sequence encodes a fusion protein comprising the extracellular
CC   domain of mouse co-stimulatory molecule B7-1 joined via a flexible
CC   peptide linker to an scFv (see AAW86002) derived from murine 5T4
CC   monoclonal antibody. The fusion can be used to construct a recombinant
CC   vector, e.g. retrovirus, lentivirus, adenovirus, poxvirus, vaccinia virus
CC   or baculovirus, used for direct treatment of tumour patients. The
CC   trophoblast cell surface antigen defined by 5T4 is expressed at high
CC   levels on the cells of a wide variety of human tumours. The invention
CC   relates to a vector comprising a nucleotide sequence coding for a tumour
CC   interacting protein (TIP) and optionally a nucleotide sequence of
CC   interest (NOI) which encodes a protein of interest (POI), the vector
CC   being capable of delivering the NOI and/or POI to the tumour recognised
CC   by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC   treat cancer, and may also used as a gene delivery system for introducing
CC   at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC   a haematopoietic cell lineage. B7-1 binds specifically to CD28 and CTLA-4
CC   present on human CD4 and CD8 cells. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

  Query Match             79.0%;  Score 576;  DB 2;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 9.6e-270;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846
```

```
Qy        61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy       121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy       181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy       241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy       301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
             |||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db      1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy       361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy       421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy       481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy       541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy       601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy       661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy       721 ATCAAACGG 729
             |||||||||
Db      1507 ATCAAACGG 1515
```

RESULT 9
AAF89732
ID AAF89732 standard; DNA; 1518 BP.
XX
AC AAF89732;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a B7 link ScFv sequence.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Example 8; Fig 5; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes a B7 link ScFv sequence. A human B7 sequence is linked to a ScFv
CC of the invention
XX
SQ Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

  Query Match   79.0%; Score 576; DB 4; Length 1518;
  Best Local Similarity 99.6%; Pred. No. 9.6e-270;
  Matches 726; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

```
Qy         1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy        61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy       121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy       181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy       241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy       301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
             |||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db      1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy       361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy       421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy       481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
```

```
                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
                |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 10
AAF89733
ID AAF89733 standard; DNA; 1796 BP.
XX
AC AAF89733;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of an Ig-5T4 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 12. .1790
FT /*tag= a
FT /transl_except= (1518. .1520, aa: Met)
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR P-PSDB; AAB83838.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Claim 9; Fig 6; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes an Ig-5T4 fusion protein
XX
SQ Sequence 1796 BP; 429 A; 539 C; 466 G; 362 T; 0 U; 0 Other;

Query Match 75.6%; Score 551; DB 4; Length 1796;
Best Local Similarity 99.6%; Pred. No. 1.4e-257;
Matches 701; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 72
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 140

Qy          73 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 200

Qy         133 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 192
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 260

Qy         193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 252
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 320

Qy         253 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 312
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 380

Qy         313 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGG 372
               |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Db         381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGG 440

Qy         373 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 432
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 500

Qy         433 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 492
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 560

Qy         493 AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 552
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 620

Qy         553 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 612
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 680

Qy         613 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 672
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740

Qy         673 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 716
               |||||||||||||||||||||||||||||||||||||||||||||
Db         741 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 784
```

RESULT 11
AAV80295
ID AAV80295 standard; cDNA; 2090 BP.
XX
AC AAV80295;
XX
DT 15-MAR-1999 (first entry)
XX
DE ScFv-IgE1 fusion construct for use in cancer gene therapy.

```
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 13; Page 64; 82pp; English.
XX
CC   This DNA sequence encodes a fusion protein comprising the human IgE1
CC   heavy constant region joined via a flexible peptide linker to an scFv
CC   (see AAW86002) derived from murine 5T4 monoclonal antibody. The fusion
CC   construct can be incorporated into a recombinant viral vector for use in
CC   gene therapy of cancer. The trophoblast cell surface antigen defined by
CC   5T4 is expressed at high levels on the cells of a wide variety of human
CC   tumours. Binding of IgE to tumour cells should promote a strong histamine
CC   and hence inflammatory response and destruction of tumour cells. The
CC   invention relates to a vector comprising a nucleotide sequence coding for
CC   a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC   of interest (NOI) which encodes a protein of interest (POI), the vector
CC   being capable of delivering the NOI and/or POI to the tumour recognised
CC   by the TIP. Delivery can be in vivo or ex vivo
XX
SQ   Sequence 2090 BP; 461 A; 653 C; 565 G; 411 T; 0 U; 0 Other;

  Query Match           75.6%;  Score 551;  DB 2;  Length 2090;
  Best Local Similarity  99.6%;  Pred. No. 1.4e-257;
  Matches  701;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 140

Qy         73 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 200

Qy        133 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 260

Qy        193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 320

Qy        253 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 380

Qy        313 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGG 372
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||

Db        381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGG 440

Qy        373 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 500

Qy        433 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 560

Qy        493 AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 552
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        561 AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 620

Qy        553 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 680

Qy        613 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740

Qy        673 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 716
              |||||||||||||||||||||||||||||||||||||||||||
Db        741 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 784


RESULT 12
AAF89734
ID   AAF89734 standard; DNA; 2090 BP.
XX
AC   AAF89734;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a SvFv-IgE protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder; ss.
XX
OS   Synthetic.
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Example 11; Fig 7; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
```

```
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a ScFv of the invention linked to an IgE sequence
XX
SQ   Sequence 2090 BP; 461 A; 654 C; 564 G; 411 T; 0 U; 0 Other;

  Query Match            75.6%;  Score 551;  DB 4;  Length 2090;
  Best Local Similarity  99.6%;  Pred. No. 1.4e-257;
  Matches  701;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         13 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT 140

Qy         73 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 200

Qy        133 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTC 260

Qy        193 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGC 320

Qy        253 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAAC 380

Qy        313 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGG 372
              |||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Db        381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCAGGTGGTGGTGGG 440

Qy        373 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACA 500

Qy        433 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG 560

Qy        493 AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 552
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        561 AGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCC 620

Qy        553 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG 680

Qy        613 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740

Qy        673 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 716
              |||||||||||||||||||||||||||||||||||||||||||||
Db        741 CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT 784


RESULT 13
AAQ73679
ID   AAQ73679 standard; DNA; 729 BP.
XX
AC   AAQ73679;
XX
DT   25-MAR-2003  (revised)
DT   09-MAY-1995  (first entry)
XX
DE   Fv(GP-4) immunosuppressive.
XX
KW   MAb; monoclonal antibody; hybridoma; interleukin-2; IL-2; Fv;
KW   antibody variable region; GP-4; Fv(GP-4); immunosuppressive; ss.
XX
OS   Mus sp.
XX
PN   EP621338-A2.
XX
PD   26-OCT-1994.
XX
PF   21-APR-1994;   94EP-00106257.
XX
PR   21-APR-1993;   93JP-00094491.
PR   07-MAR-1994;   94JP-00036065.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
PI   Shimamura T,  Hamura J,  Nakazawa H,  Kanayama Y,  Sugamura K;
PI   Takeshita T;
XX
DR   WPI; 1994-325948/41.
DR   P-PSDB; AAR60781.
XX
PT   Immunosuppressant polypeptide - has ability to block interleukin-2
PT   response.
XX
PS   Claim 18; Page 29; 37pp; English.
XX
CC   MAb capable of binding to the gamma chain of the IL-2 receptor, and thus
CC   of blocking the IL-2 response, is produced by mouse hybridoma line GP-4
CC   (FERM BP-4640). DNA encoding the variable region of this MAb was
CC   expressed in E. coli, yielding Fv(GP-4) with immumosuppressive activity.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 729 BP; 199 A; 169 C; 182 G; 179 T; 0 U; 0 Other;

  Query Match            11.8%;  Score 86;  DB 2;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-31;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 456

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
              |||||||||||||||||||||||||
Db        457 GGCTACTACATGCACTGGGTGAAGCA 482


RESULT 14
ADM72026
ID   ADM72026 standard; DNA; 1413 BP.
XX
AC   ADM72026;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Chimeric mouse-human antibody M1E07 heavy chain encoding DNA.
XX
KW   GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW   cytostatic; gene; ds; M1E07.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1413
FT                   /*tag=  a
FT                   /product= "M1E07 heavy chain"
XX
PN   WO2004022739-A1.
```

```
XX
PD   18-MAR-2004.
XX
PF   04-SEP-2003; 2003WO-JP011318.
XX
PR   04-SEP-2002; 2002WO-JP008999.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Aburatani H,  Midorikawa Y,  Nakano K,  Ohizumi I,  Ito Y,  Tokita S;
XX
DR   WPI; 2004-269573/25.
DR   P-PSDB; ADM72027.
XX
PT   Antibody against the N terminus of glypican 3(GPC3) causes cell
PT   disruption and is useful as an anticancer agent.
XX
PS   Example 4; SEQ ID NO 11; 122pp; Japanese.
XX
CC   The invention relates to an antibody against the N terminus of glypican 3
CC   (GPC3). The antiboduy can be used for causing cell disruption and can be
CC   uses as an anti-cancer agent. The present sequence represents a chimeric
CC   mouse-human antibody M1E07 heavy chain encoding DNA.
XX
SQ   Sequence 1413 BP; 340 A; 436 C; 372 G; 265 T; 0 U; 0 Other;

  Query Match             11.8%;  Score 86;  DB 12;  Length 1413;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-31;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 147

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
               ||||||||||||||||||||||||||
Db        148 GGCTACTACATGCACTGGGTGAAGCA 173


RESULT 15
AAT43737
ID   AAT43737 standard; cDNA; 334 BP.
XX
AC   AAT43737;
XX
DT   27-AUG-2003  (revised)
DT   12-AUG-1997  (first entry)
XX
DE   Anti-DNA antibody 7b3 heavy chain variable region cDNA.
XX
KW   Heavy chain; variable region; anti-DNA; monoclonal; antibody; MAb 7b3;
KW   hairpin; diagnosis; inflammatory glomerulonephritis;
KW   systemic lupus erythematosus; screening; treatment; prevention; SLE;
KW   disease; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .334
FT                   /*tag= a
FT                   /note= "no STOP codon given"
XX
PN   WO9636361-A1.
XX
PD   21-NOV-1996.
XX
PF   16-MAY-1996;   96WO-US007113.
XX
PR   18-MAY-1995;   95US-00443540.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Glick GD,  Swanson PC;
XX
DR   WPI; 1997-011854/01.
XX
PT   Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT   develop prods. for diagnosis and treatment of disorders, e.g.
PT   glomerulonephritis or systemic lupus erythematosus.
XX
PS   Example; Fig 7; 102pp; English.
XX
CC   The present sequence encodes the heavy chain variable region of the anti-
CC   DNA monoclonal antibody (MAb) 7b3, which has a high affinity for single
CC   stranded DNA, low or no affinity for double stranded DNA and specifically
CC   binds a DNA hairpin. The MAb can be used diagnose disorders associated
CC   with the pathological complexation of DNA, e.g. inflammatory
CC   glomerulonephritis and systemic lupus erythematosus. It can also be used
CC   to generate reagents to screen for pharmaceutical agents, and treat
CC   and/or prevent an above disorder. Calf thymus DNA was used to immunise a
CC   MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma
CC   cells to give hybridomas producing the anti-DNA MAb. 7b3 was found to
CC   react strongly with poly(dT), poly(dG) and poly(dI), moderately with
CC   single stranded DNA and weakly with poly(G). (Updated on 27-AUG-2003 to
CC   correct OS field.)
XX
SQ   Sequence 334 BP; 93 A; 79 C; 83 G; 79 T; 0 U; 0 Other;

  Query Match              9.1%;  Score 66;  DB 2;  Length 334;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-21;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 67

Qy         91 GGCTAC 96
               ||||||
Db         68 GGCTAC 73


Search completed: March 15, 2005, 21:19:17
Job time : 591 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 20:44:30 ; Search time 236 Seconds
(without alignments)
5054.431 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	11.8	729	1	US-08-230-843-3	Sequence 3, Appli
2	86	11.8	729	2	US-08-636-936-3	Sequence 3, Appli
3	66	9.1	334	3	US-08-881-037-11	Sequence 11, Appl
4	63	8.6	906	2	US-08-656-906-24	Sequence 24, Appl
5	63	8.6	906	3	US-09-217-847-24	Sequence 24, Appl
6	62	8.5	318	1	US-08-463-128-2	Sequence 2, Appli
7	62	8.5	318	1	US-08-463-298-2	Sequence 2, Appli
8	62	8.5	318	2	US-08-436-339A-2	Sequence 2, Appli
9	62	8.5	318	2	US-08-822-830B-3	Sequence 3, Appli
10	62	8.5	318	2	US-08-950-660-3	Sequence 3, Appli
11	62	8.5	318	4	US-09-157-452B-3	Sequence 3, Appli
12	62	8.5	318	4	US-08-454-899G-9	Sequence 9, Appli
13	62	8.5	318	5	PCT-US93-00030-3	Sequence 3, Appli
14	62	8.5	318	5	PCT-US93-00924-3	Sequence 3, Appli
15	62	8.5	318	5	PCT-US94-10395-2	Sequence 2, Appli
16	59	8.1	714	3	US-09-142-974B-2	Sequence 2, Appli
17	59	8.1	1173	3	US-09-142-974B-4	Sequence 4, Appli
18	56	7.7	405	1	US-08-137-117D-26	Sequence 26, Appl
19	56	7.7	405	1	US-08-436-717-26	Sequence 26, Appl
20	56	7.7	1425	4	US-09-592-998C-6	Sequence 6, Appli
21	52	7.1	344	2	US-08-888-366-7	Sequence 7, Appli
22	52	7.1	372	3	US-09-257-069-1	Sequence 1, Appli
23	52	7.1	372	4	US-10-007-790-1	Sequence 1, Appli
24	52	7.1	405	1	US-08-398-613A-49	Sequence 49, Appl
25	52	7.1	405	1	US-08-398-612A-49	Sequence 49, Appl
26	52	7.1	405	1	US-08-398-611A-49	Sequence 49, Appl
27	52	7.1	405	1	US-08-396-851A-49	Sequence 49, Appl
28	52	7.1	405	2	US-08-491-334A-49	Sequence 49, Appl
29	52	7.1	405	3	US-09-027-449-36	Sequence 36, Appl
30	52	7.1	405	3	US-08-804-444A-36	Sequence 36, Appl
31	52	7.1	405	3	US-09-026-985-36	Sequence 36, Appl
32	52	7.1	405	3	US-09-121-952A-36	Sequence 36, Appl
33	52	7.1	405	3	US-09-234-340A-36	Sequence 36, Appl
34	52	7.1	738	1	US-08-197-834-6	Sequence 6, Appli
35	52	7.1	762	1	US-08-398-613A-57	Sequence 57, Appl
36	52	7.1	762	1	US-08-398-612A-57	Sequence 57, Appl
37	52	7.1	762	1	US-08-398-611A-57	Sequence 57, Appl
38	52	7.1	762	1	US-08-396-851A-57	Sequence 57, Appl
39	52	7.1	762	2	US-08-491-334A-57	Sequence 57, Appl
40	52	7.1	762	3	US-09-027-449-43	Sequence 43, Appl
41	52	7.1	762	3	US-08-804-444A-43	Sequence 43, Appl
42	52	7.1	762	3	US-09-026-985-43	Sequence 43, Appl
43	52	7.1	762	3	US-09-121-952A-43	Sequence 43, Appl
44	52	7.1	762	3	US-09-234-340A-43	Sequence 43, Appl
45	51	7.0	324	4	US-09-486-814A-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-08-230-843-3
; Sequence 3, Application US/08230843
; Patent No. 5582826
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMAMURA, TOSHIRO
;    APPLICANT:  HAMURO, JUNJI
;    APPLICANT:  NAKAZAWA, HARUMI
;    APPLICANT:  KANAYAMA, YUKA
;    APPLICANT:  SUGAMURA, KAZUO
;    APPLICANT:  TAKESHITA, TOSHIKAZU
;    TITLE OF INVENTION:  IMMUNOSUPPRESSANT
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/230,843
;      FILING DATE:  21-APR-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 094491/1993
;      FILING DATE:  21-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 036065/1994
;      FILING DATE:  07-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5582826man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  0010-0674-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  729 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  Other nucleic acid
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..729
US-08-230-843-3

  Query Match            11.8%;  Score 86;  DB 1;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 1e-33;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 456

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
              ||||||||||||||||||||||||||
Db        457 GGCTACTACATGCACTGGGTGAAGCA 482


RESULT 2
US-08-636-936-3
; Sequence 3, Application US/08636936
; Patent No. 5856140
;  GENERAL INFORMATION:
;    APPLICANT:  SHIMAMURA, TOSHIRO
;    APPLICANT:  HAMURO, JUNJI
;    APPLICANT:  NAKAZAWA, HARUMI
;    APPLICANT:  KANAYAMA, YUKA
;    APPLICANT:  SUGAMURA, KAZUO
;    APPLICANT:  TAKESHITA, TOSHIKAZU
;    TITLE OF INVENTION:  IMMUNOSUPPRESSANT
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/636,936
;      FILING DATE:  24-APR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/230,843
;      FILING DATE:  21-APR-1994
;      APPLICATION NUMBER:  JP 094491/1993
;      FILING DATE:  21-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 036065/1994
;      FILING DATE:  07-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5856140man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  0010-0674-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  729 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..729
US-08-636-936-3

  Query Match            11.8%;  Score 86;  DB 2;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 1e-33;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 456

Qy         91 GGCTACTACATGCACTGGGTGAAGCA 116
              ||||||||||||||||||||||||||
Db        457 GGCTACTACATGCACTGGGTGAAGCA 482


RESULT 3
US-08-881-037-11
; Sequence 11, Application US/08881037
; Patent No. 6080588
;  GENERAL INFORMATION:
;    APPLICANT:  Glick, Gary D.
;    APPLICANT:  Swanson, Patrick C.
;    TITLE OF INVENTION:  DNA BINDING ANTIBODIES
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,037
;      FILING DATE:  23-JUN-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/443,540
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Konski, Antoinette F.
;      REGISTRATION NUMBER:  34,202
;      REFERENCE/DOCKET NUMBER:  203442110710
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-881-037-11

  Query Match            9.1%;  Score 66;  DB 3;  Length 334;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-23;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 67

Qy         91 GGCTAC 96
              ||||||
Db         68 GGCTAC 73
```

```
RESULT 4
US-08-656-906-24
; Sequence 24, Application US/08656906
; Patent No. 5972901
;  GENERAL INFORMATION:
;    APPLICANT:  Ferkol Jr., Thomas W.
;    APPLICANT:  Davis, Pamela B.
;    APPLICANT:  Ziady, Assem-Galal
;    TITLE OF INVENTION:  Serpin Enzyme Complex Receptor -
;    TITLE OF INVENTION:  Mediated Gene Transfer
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/656,906
;      FILING DATE:  03-JUN-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/
;      FILING DATE:  03-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO WO 95/25809
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/216,534
;      FILING DATE:  23-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  CASE-02280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  906 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..906
US-08-656-906-24

  Query Match             8.6%;  Score 63;  DB 2;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-22;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 444

Qy         67 AAG 69
              |||
Db        445 AAG 447


RESULT 5
US-09-217-847-24
; Sequence 24, Application US/09217847
; Patent No. 6200801
;  GENERAL INFORMATION:
;    APPLICANT:  Ferkol Jr., Thomas W.
;    APPLICANT:  Davis, Pamela B.
;    APPLICANT:  Ziady, Assem-Galal
;    TITLE OF INVENTION:  Serpin Enzyme Complex Receptor -
;    TITLE OF INVENTION:  Mediated Gene Transfer
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States Of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/217,847
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/656,906
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO WO 95/25809
;      FILING DATE:  23-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/216,534
;      FILING DATE:  23-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ingolia, Diane E.
;      REGISTRATION NUMBER:  40,027
;      REFERENCE/DOCKET NUMBER:  CASE-02280
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  906 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..906
US-09-217-847-24

  Query Match             8.6%;  Score 63;  DB 3;  Length 906;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-22;
  Matches   63;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 444

Qy         67 AAG 69
              |||
Db        445 AAG 447


RESULT 6
US-08-463-128-2
; Sequence 2, Application US/08463128
; Patent No. 5695755
;  GENERAL INFORMATION:
;    APPLICANT:  Papayannopoulou, Thalia (USA only)
;    APPLICANT:  Board of Regents, U.
;    APPLICANT:  Washington (except USA)
```

```
;    TITLE OF INVENTION:  PERIPHERALIZATION OF HEMATOPOIETIC STEM
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,128
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11060
;      FILING DATE:  11-11-1993
;      APPLICATION NUMBER:  US 07/977,702
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B173CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-128-2

  Query Match             8.5%;  Score 62;  DB 1;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 7
US-08-463-298-2
; Sequence 2, Application US/08463298
; Patent No. 5824304
;  GENERAL INFORMATION:
;    APPLICANT:  Papayannopoulou, Thalia (USA only)
;    APPLICANT:  Board of Regents, U.
;    APPLICANT:  Washington (except USA)
;    TITLE OF INVENTION:  PERIPHERALIZATION OF HEMATOPOIETIC STEM
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,298
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11060
;      FILING DATE:  11-NOV-1993
;      APPLICATION NUMBER:  US 07/977,702
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B173CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-463-298-2

  Query Match             8.5%;  Score 62;  DB 1;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 8
US-08-436-339A-2
; Sequence 2, Application US/08436339A
; Patent No. 5843438
;  GENERAL INFORMATION:
;    APPLICANT:  Papayannopoulou, Thalia (USA only)
;    APPLICANT:  Board of Regents, U.
;    APPLICANT:  Washington (except USA)
;    TITLE OF INVENTION:  PERIPHERALIZATION OF HEMATOPOIETIC STEM
;    TITLE OF INVENTION:  CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  c/o FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,339A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/463,128
;      FILING DATE:  05-JUN-1995
;      APPLICATION NUMBER:  PCT/US93/11060
;      FILING DATE:  11-11-1993
;      APPLICATION NUMBER:  US 07/977,702
;      FILING DATE:  13-NOV-1992
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  B173CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 596-9000
;      TELEFAX:  (212) 596-9090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-339A-2

  Query Match             8.5%;  Score 62;  DB 2;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 9
US-08-822-830B-3
; Sequence 3, Application US/08822830B
; Patent No. 5871734
;  GENERAL INFORMATION:
;    APPLICANT:  Lobb, Roy R.; Burkly, Linda C.
;    TITLE OF INVENTION:  Treatment for Asthma with VLA-4 Blocking
;    TITLE OF INVENTION:  Agents
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,830B
;      FILING DATE:  03-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/456,193
;      FILING DATE:  31-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/374,331
;      FILING DATE:  18-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/256,631
;      FILING DATE:  12-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00030
;      FILING DATE:  12-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/821,768
;      FILING DATE:  13-JAN 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Louis (PLM)
;      REGISTRATION NUMBER:  35,965
;      REFERENCE/DOCKET NUMBER:  BGP-021USCN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..318
;      OTHER INFORMATION:  /note= "HP1/2 light chain variable
;      OTHER INFORMATION:  region"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pBAG172 insert: HP1/2 light
;      OTHER INFORMATION:  chain variable region"
US-08-822-830B-3

  Query Match             8.5%;  Score 62;  DB 2;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 10
US-08-950-660-3
; Sequence 3, Application US/08950660
; Patent No. 5932214
;  GENERAL INFORMATION:
;    APPLICANT:  Lobb, Roy R.; Burkly, Linda C.
;    TITLE OF INVENTION:  Treatment For Inflammatory Bowel Disease
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/950,660
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/456,124
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/373,857
;      FILING DATE:  18-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/284,603
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00924
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/835,139
;      FILING DATE:  12-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Louis (PLM)
;      REGISTRATION NUMBER:  35,965
```

```
;       REFERENCE/DOCKET NUMBER:  BGP-031USCP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  318 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..318
;       OTHER INFORMATION:  /note= "HP1/2 light chain variable
;       OTHER INFORMATION:  region"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1
;       OTHER INFORMATION:  /note= "pBAG172 insert: HP1/2 light
;       OTHER INFORMATION:  chain variable region"
US-08-950-660-3

  Query Match             8.5%;  Score 62;  DB 2;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 11
US-09-157-452B-3
; Sequence 3, Application US/09157452B
; Patent No. 6482409
; GENERAL INFORMATION:
;  APPLICANT: Lobb, Roy R.
;  APPLICANT:  Burkly, Linda C.
;  TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
;  FILE REFERENCE: 10274-004003
;  CURRENT APPLICATION NUMBER: US/09/157,452B
;  CURRENT FILING DATE:  1998-09-21
;  PRIOR APPLICATION NUMBER: US 08/950,660
;  PRIOR FILING DATE: 1997-10-15
;  PRIOR APPLICATION NUMBER: US 08/373,857
;  PRIOR FILING DATE: 1995-01-18
;  PRIOR APPLICATION NUMBER: US 08/284,603
;  PRIOR FILING DATE: 1994-08-11
;  PRIOR APPLICATION NUMBER: PCT/US93/00924
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: US 07/835,139
;  PRIOR FILING DATE: 1992-02-12
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 318
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(318)
;   NAME/KEY: misc_feature
;   LOCATION: (1)
;   OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
US-09-157-452B-3

  Query Match             8.5%;  Score 62;  DB 4;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 12
US-08-454-899G-9
; Sequence 9, Application US/08454899G
; Patent No. 6602503
; GENERAL INFORMATION:
;  APPLICANT: Lobb, Roy R.
;  APPLICANT:  Carr, Frank J.
;  APPLICANT:  Tempest, Philip R.
;  TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
;  FILE REFERENCE: 10274-007001
;  CURRENT APPLICATION NUMBER: US/08/454,899G
;  CURRENT FILING DATE:  1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/004,798
;  PRIOR FILING DATE: 1993-01-12
;  PRIOR APPLICATION NUMBER: PCT/US94/00266
;  PRIOR FILING DATE: 1994-01-07
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 318
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: light chain variable region
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(318)
US-08-454-899G-9

  Query Match             8.5%;  Score 62;  DB 4;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 13
PCT-US93-00030-3
; Sequence 3, Application PC/TUS9300030
;  GENERAL INFORMATION:
;    APPLICANT:  Lobb, Roy R.
;    TITLE OF INVENTION:  Treatment for Asthma
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  PCT/US93/00030
;      FILING DATE:  19930112
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  92,307-A; D002 CIP PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..318
;      OTHER INFORMATION:  /product= "HP1/2 light chain
;      OTHER INFORMATION:  variable region"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pBAG172 insert: HP1/2 light
;      OTHER INFORMATION:  chain variable region"
PCT-US93-00030-3

  Query Match              8.5%;  Score 62;  DB 5;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 14
PCT-US93-00924-3
; Sequence 3, Application PC/TUS9300924
;  GENERAL INFORMATION:
;    APPLICANT:  Lobb, Roy R.
;    TITLE OF INVENTION:  Treatment for Inflammatory Bowel Disease
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allegretti & Witcoff, Ltd.
;      STREET:  10 South Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00924
;      FILING DATE:  19930202
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  92,308-A; D003 CIP PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-715-1000
;      TELEFAX:  312-715-1234
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  318 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..318
;      OTHER INFORMATION:  /product= "HP1/2 light chain
;      OTHER INFORMATION:  variable region"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pBAG172 insert: HP1/2 light
;      OTHER INFORMATION:  chain variable region"
PCT-US93-00924-3

  Query Match              8.5%;  Score 62;  DB 5;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


RESULT 15
PCT-US94-10395-2
; Sequence 2, Application PC/TUS9410395
;  GENERAL INFORMATION:
;    APPLICANT:  EMORY UNIVERSITY
;    APPLICANT:  GEORGIA TECH RESEARCH CORPORATION
;    APPLICANT:  SWERLICK, Robert A.
;    APPLICANT:  ECKMAN, James R.
;    APPLICANT:  WICK, Timothy M.
;    TITLE OF INVENTION:  Method of Inhibiting Binding of
;    TITLE OF INVENTION:  Reticulocytes to Endothelium by
;    TITLE OF INVENTION:  Interfering with VLA-4/VCAM-1
;    TITLE OF INVENTION:  Interactions
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leslie M. Levine
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10395
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/122,228
;      FILING DATE:  15-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Levine, Leslie M.
;      REGISTRATION NUMBER:  35,245
;      REFERENCE/DOCKET NUMBER:  D017CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 252-9810
;      TELEFAX:  (617) 252-9617
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  318 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US94-10395-2

  Query Match             8.5%;  Score 62;  DB 5;  Length 318;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-21;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86

Qy        492 GA 493
              ||
Db         87 GA 88


Search completed: March 15, 2005, 23:24:20
Job time : 239 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:45:28 ; Search time 74 Seconds
(without alignments)
1270.037 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....QQDYNSPPTFGGGTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1279	100.0	243	2	AAW86002	Aaw86002 Murine an
2	1279	100.0	243	2	AAY42294	Aay42294 Anti-5T4
3	1279	100.0	243	2	AAY27407	Aay27407 5T4 scFv
4	1279	100.0	243	4	AAB83835	Aab83835 Amino aci
5	1279	100.0	592	4	AAB83838	Aab83838 Amino aci
6	1279	100.0	595	2	AAW86003	Aaw86003 Anti-5T4
7	1274	99.6	488	2	AAW86004	Aaw86004 Human B7-
8	1274	99.6	488	4	AAB83836	Aab83836 Amino aci
9	1274	99.6	488	6	ABU07262	Abu07262 Human exp
10	1274	99.6	488	6	ABU07253	Abu07253 Human exp
11	972.5	76.0	672	6	ABP58454	Abp58454 Engineere
12	935	73.1	267	8	ADR70320	Adr70320 Polioviru
13	903.5	70.6	580	2	AAW90217	Aaw90217 Bispecifi
14	897.5	70.2	556	2	AAW90218	Aaw90218 Bispecifi
15	889.5	69.5	244	8	ADG17481	Adg17481 Anti-CD22
16	889	69.5	249	1	AAP80154	Aap80154 Biosynthe
17	886.5	69.3	244	8	ADG17480	Adg17480 Anti-CD22
18	883.5	69.1	244	8	ADG17477	Adg17477 Anti-CD22
19	883	69.0	288	2	AAW82743	Aaw82743 Fusion pr
20	883	69.0	673	2	AAW82742	Aaw82742 Plasmid p
21	880.5	68.8	244	8	ADG17482	Adg17482 Anti-CD22
22	880.5	68.8	244	8	ADG17478	Adg17478 Anti-CD22
23	879	68.7	895	5	AAU75369	Aau75369 Diphtheri
24	879	68.7	895	5	AAU75368	Aau75368 Diphtheri
25	879	68.7	895	5	AAU75374	Aau75374 Diphtheri
26	879	68.7	895	6	AAO29673	Aao29673 Anti-T ce
27	879	68.7	896	5	AAU75367	Aau75367 Diphtheri
28	879	68.7	896	5	AAU75366	Aau75366 Diphtheri
29	879	68.7	896	5	AAU75373	Aau75373 Diphtheri
30	879	68.7	896	6	AAO29672	Aao29672 Anti-T ce
31	879	68.7	896	6	AAO29671	Aao29671 Anti-T ce
32	879	68.7	896	6	AAO29676	Aao29676 Anti-T ce
33	879	68.7	899	5	AAU75375	Aau75375 Diphtheri
34	879	68.7	899	6	AAO29674	Aao29674 Anti-T ce
35	878	68.6	311	2	AAR05378	Aar05378 Multifunc
36	878	68.6	313	1	AAB62305	Aab62305 Single ch
37	877.5	68.6	244	8	ADG17484	Adg17484 Anti-CD22
38	876	68.5	283	8	ADF85426	Adf85426 V122scFv
39	875.5	68.5	244	8	ADG17479	Adg17479 Anti-CD22
40	875.5	68.5	244	8	ADG17483	Adg17483 Anti-CD22
41	875.5	68.5	244	8	ADG17486	Adg17486 Anti-CD22
42	874	68.3	291	6	ABR42054	Abr42054 Newcastle
43	872.5	68.2	244	8	ADG17487	Adg17487 Anti-CD22
44	872.5	68.2	244	8	ADG17485	Adg17485 Anti-CD22
45	870	68.0	311	1	AAP80151	Aap80151 Multifunc

ALIGNMENTS

RESULT 1
AAW86002
ID AAW86002 standard; protein; 243 AA.
XX
AC AAW86002;
XX
DT 15-MAR-1999 (first entry)
XX
DE Murine anti-5T4 antigen monoclonal antibody scFv.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Misc-difference 169
FT /note= "encoded by GDT"
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR N-PSDB; AAV80290.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1A; 82pp; English.
XX
CC This amino acid sequence comprises an scFv, termed 5T4scFv.1, comprising
CC the heavy chain variable region (VH) from the murine 5T4 monoclonal
CC antibody followed by a 15-amino acid flexible linker and the light chain
CC variable region (VL) of the mouse 5T4 antibody. The trophoblast cell

CC surface antigen defined by monoclonal antibody 5T4 is expressed at high
CC levels on the cells of a wide variety of human tumours. 5T4scFv.1 DNA
CC (see AAV80290) can be used to construct single-chain antibodies (see
CC AAW86003) and scFv fusion constructs (see AAW86004-05). The invention
CC relates to a vector comprising a nucleotide sequence coding for a tumour
CC interacting protein (TIP) and optionally a nucleotide sequence of
CC interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC treat cancer, and may also used as a gene delivery system for introducing
CC at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 7.5e-84;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240

Qy        241 IKR 243
              |||
Db        241 IKR 243
```

RESULT 2
AAY42294
ID AAY42294 standard; protein; 243 AA.
XX
AC AAY42294;
XX
DT 06-DEC-1999 (first entry)
XX
DE Anti-5T4 secreted single chain antibody Fv fragment.
XX
KW Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
KW nucleus.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9945127-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB000674.
XX
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-551046/46.
DR N-PSDB; AAZ19786.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors.
XX
PS Example 9; Fig 3; 187pp; English.
XX
CC This sequence represents an example of a secreted single chain antibody
CC Fv fragment (in this case, directed against the 5T4 antigen), which is
CC involved in transcellular localisation. A secreted single chain antibody
CC Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives
CC such as anchorless P450R (AAY42287) or FN fragment (AAY42288). This
CC enables the fusion protein to be delivered to other cells where it is
CC then transported to the nucleus. Many drugs' sites of action are in the
CC nucleus, rather than the cytoplasm, where P450R normally functions. P450R
CC or its derivatives can be used to activate prodrugs to their active form
CC via reduction. Administration of a prodrug is useful where the active
CC drug may be metabolised before it reaches its site of action or where the
CC active drug is cytotoxic, e.g., anticancer drugs. Targetted delivery of
CC such prodrug activators allows a reduction in dose of the prodrug, and
CC thus of systemic side-effects. P450R derivative fusion proteins, or
CC vectors that express them, are specifically used to treat tumours,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g., cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, ischaemia or
CC hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anaesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 1279; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 7.5e-84;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240

Qy        241 IKR 243
              |||
Db        241 IKR 243
```

RESULT 3
AAY27407
ID AAY27407 standard; protein; 243 AA.
XX
AC AAY27407;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody signal peptide.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
KW 5T4 scFv.
XX
OS Unidentified.
XX

```
PN   WO9945126-A2.
XX
PD   10-SEP-1999.
XX
PF   05-MAR-1999;   99WO-GB000672.
XX
PR   06-MAR-1998;   98GB-00004841.
PR   19-AUG-1998;   98GB-00018103.
PR   29-JAN-1999;   99GB-00002081.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Stratford IJ,  Patterson AV,  Kingsman SM,  Kan O,  Griffiths L;
PI   Mitrophanous K;
XX
DR   WPI; 1999-540852/45.
DR   N-PSDB; AAZ07810.
XX
PT   New prodrug activating agent targeted to selected cells or tissues,
PT   particularly hypoxic cells, for treating e.g. tumors or inflammation.
XX
PS   Example 9; Fig 3F; 149pp; English.
XX
CC   The invention provides a new prodrug activating agent that comprises: (i)
CC   a localization domain (LD; other than a tumor-selective antibody) and a
CC   prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC   a cytochrome P450 and under control of at least one constitutive or
CC   inducible expression control sequence or (iii) a modified hematopoietic
CC   stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC   under control of elements as in (ii). The prodrug activating agent or
CC   vectors that express them, are specifically used to treat tumors,
CC   inflammation, atherosclerosis and muscular dystrophy, but may also be
CC   used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC   arthritis, or conditions associated with hypoxia, hypoglycemia or
CC   ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC   anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC   agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC   locations or by delivering it to neighboring cells (bystander effect),
CC   and allow a reduction in dose of prodrug, and thus of systemic side-
CC   effects. Nucleic acids encoding the agent may be expressed selectively in
CC   hypoxic cells. The present sequence represents the single chain variable
CC   antibody fragment against the tumor antigen 5T4 (5T4 scFv). 5T4 scFv is
CC   used in the construction of a fusion protein comprising 5T4 scFv and a
CC   human P450 reductase derivative alP450R
XX
SQ   Sequence 243 AA;

  Query Match             100.0%;  Score 1279;  DB 2;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-84;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240

Qy        241 IKR 243
              |||
Db        241 IKR 243


RESULT 4
AAB83835
ID   AAB83835 standard; protein; 243 AA.
XX
AC   AAB83835;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 169
FT                   /note= "Ala encoded by GDT"
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   N-PSDB; AAF89729.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Claim 3; Fig 1; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   represents a 5T4 ScFv of the invention. The antibody comprises the VH and
CC   VL regions from murine 5T4 monoclonal antibody, joined by a linker
CC   sequence
XX
SQ   Sequence 243 AA;

  Query Match             100.0%;  Score 1279;  DB 4;  Length 243;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-84;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120

Qy         121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180

Qy         181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240

Qy         241 IKR 243
                |||
Db         241 IKR 243


RESULT 5
AAB83838
ID   AAB83838 standard; protein; 592 AA.
XX
AC   AAB83838;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of an Ig-5T4 fusion protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 503
FT                   /note= "Met encoded by CTG"
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   N-PSDB; AAF89733.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Disclosure; Fig 6; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   represents an Ig-5T4 fusion protein
XX
SQ   Sequence 592 AA;

  Query Match             100.0%;  Score 1279;  DB 4;  Length 592;
  Best Local Similarity   100.0%;  Pred. No. 2e-83;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          20 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 79

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          80 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 139

Qy         121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         140 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 199

Qy         181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         200 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 259

Qy         241 IKR 243
                |||
Db         260 IKR 262


RESULT 6
AAW86003
ID   AAW86003 standard; protein; 595 AA.
XX
AC   AAW86003;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Anti-5T4 single chain antibody 5T4Sab1.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; mouse; human; 5T4Sab1.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
DR   N-PSDB; AAV80291.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 1; Fig 1B; 82pp; English.
XX
CC   This is the amino acid sequence of a single chain antibody (Sab), termed
```

```
CC   5T4Sab1, comprising an scFv derived from murine monoclonal antibody 5T4
CC   (see AAW86002) and the human g1 constant region. cDNA (see AAV80291)
CC   encoding the Sab has been inserted into vector pCIneo to allow expression
CC   in mammalian cells. The trophoblast cell surface antigen defined by 5T4
CC   is expressed at high levels on the cells of a wide variety of human
CC   tumours. The invention relates to a vector comprising a nucleotide
CC   sequence coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI) which encodes a protein of interest
CC   (POI), the vector being capable of delivering the NOI and/or POI to the
CC   tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC   vector is used to treat cancer, and may also used as a gene delivery
CC   system for introducing at least 1 gene encoding a TIP (preferably a
CC   tumour binding protein) into a haematopoietic cell lineage
XX
SQ   Sequence 595 AA;

  Query Match             100.0%;  Score 1279;  DB 2;  Length 595;
  Best Local Similarity   100.0%;  Pred. No. 2e-83;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 82

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 142

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 202

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 262

Qy        241 IKR 243
              |||
Db        263 IKR 265


RESULT 7
AAW86004
ID   AAW86004 standard; protein; 488 AA.
XX
AC   AAW86004;
XX
DT   15-MAR-1999  (first entry)
XX
DE   Human B7-1.5T4.1 protein fusion, specific for human 5T4.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; mouse; human; B7-1;
KW   co-stimulatory molecule.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
DR   N-PSDB; AAV80292.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 5; Fig 2; 82pp; English.
XX
CC   This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC   comprising the extracellular domain (amino acids 1-215) of human co-
CC   stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC   (see AAW86002) derived from murine 5T4 monoclonal antibody. B7-1.5T4.1
CC   cDNA (see AAV80292) can be inserted into vector pCI to allow expression
CC   of the fusion protein in mammalian cells. The trophoblast cell surface
CC   antigen defined by 5T4 is expressed at high levels on the cells of a wide
CC   variety of human tumours. The invention relates to a vector comprising a
CC   nucleotide sequence coding for a tumour interacting protein (TIP) and
CC   optionally a nucleotide sequence of interest (NOI) which encodes a
CC   protein of interest (POI), the vector being capable of delivering the NOI
CC   and/or POI to the tumour recognised by the TIP. Delivery can be in vivo
CC   or ex vivo. The vector is used to treat cancer, and may also used as a
CC   gene delivery system for introducing at least 1 gene encoding a TIP
CC   (preferably a tumour binding protein) into a haematopoietic cell lineage.
CC   B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human
CC   T-cells
XX
SQ   Sequence 488 AA;

  Query Match             99.6%;  Score 1274;  DB 2;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-83;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 306

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 366

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 486

Qy        241 IK 242
              ||
Db        487 IK 488


RESULT 8
AAB83836
ID   AAB83836 standard; protein; 488 AA.
XX
AC   AAB83836;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Amino acid sequence of a B7-1.5T4.1 fusion protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder.
XX
OS   Synthetic.
OS   Mus sp.
```

OS Homo sapiens.
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR N-PSDB; AAF89730.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Claim 3; Fig 2; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC represents a B7-1.5T4.1 fusion protein. This comprises the N-terminus of
CC the 5T4 ScFv is fused after amino acid 215 of human B7-1
XX
SQ Sequence 488 AA;

Query Match 99.6%; Score 1274; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.7e-83;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 306

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 366

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 486

Qy        241 IK 242
              ||
Db        487 IK 488
```

RESULT 9
ABU07262
ID ABU07262 standard; protein; 488 AA.
XX
AC ABU07262;

XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1963.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1963; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 488 AA;

Query Match 99.6%; Score 1274; DB 6; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.7e-83;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 306

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 366

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 486

Qy        241 IK 242
              ||
Db        487 IK 488
```

RESULT 10
ABU07253
ID ABU07253 standard; protein; 488 AA.
XX
AC ABU07253;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1954.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatability complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicz RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1954; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 488 AA;

```
  Query Match             99.6%;  Score 1274;  DB 6;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-83;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 306

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 366

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 486

Qy        241 IK 242
              ||
Db        487 IK 488
```

RESULT 11
ABP58454
ID ABP58454 standard; protein; 672 AA.
XX
AC ABP58454;
XX
DT 14-APR-2003 (first entry)
XX
DE Engineered superantigen for human cancer therapy.
XX
KW Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
XX
OS Homo sapiens.
OS Staphylococcus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key   Location/Qualifiers
FT Region   1. .120
FT   /note= "5T4 variable heavy chain"
FT Misc-difference 41
FT   /note= "wild-type His substituted by Pro"
FT Misc-difference 44
FT   /note= "wild-type Ser substituted by Gly"
FT Misc-difference 69
FT   /note= "wild-type Ile substituted by Thr"
FT Misc-difference 113
FT   /note= "wild-type Val substituted by Gly"
FT Region   121. .222
FT   /note= "C242 constant heavy chain"
FT Region   226. .458
FT   /note= "SEA/E-120"
FT Misc-difference 245
FT   /note= "wild-type Arg substituted by Gly"
FT Misc-difference 246
FT   /note= "wild-type Asn substituted by Thr"
FT Misc-difference 249
FT   /note= "wild-type Ser substituted by Gly"
FT Misc-difference 252
FT   /note= "wild-type Arg substituted by Lys"
FT Misc-difference 304
FT   /note= "wild-type Lys substituted by Glu"
FT Misc-difference 306
FT   /note= "wild-type Lys substituted by Glu"
FT Misc-difference 308

```
FT                   /note= "wild-type Lys substituted by Ser"
FT   Misc-difference 309
FT                   /note= "wild-type Lys substituted by Ser"
FT   Misc-difference 452
FT                   /note= "wild-type Asp substituted by Ser"
FT   Region          459. .565
FT                   /note= "5T4 variable light chain"
FT   Misc-difference 469
FT                   /note= "wild-type Phe substituted by Ser"
FT   Misc-difference 504
FT                   /note= "wild-type Thr substituted by Lys"
FT   Misc-difference 522
FT                   /note= "wild-type Ile substituted by Ser"
FT   Misc-difference 532
FT                   /note= "wild-type Phe substituted by Leu"
FT   Misc-difference 536
FT                   /note= "wild-type Thr substituted by Ser"
FT   Misc-difference 537
FT                   /note= "wild-type Leu substituted by Val"
FT   Misc-difference 542
FT                   /note= "wild-type Leu substituted by Ala"
FT   Region          566. .672
FT                   /note= "C242 constant light chain"
XX
PN   WO2003002143-A1.
XX
PD   09-JAN-2003.
XX
PF   19-JUN-2002; 2002WO-SE001188.
XX
PR   28-JUN-2001; 2001SE-00002327.
XX
PA   (ACTI-) ACTIVE BIOTECH AB.
XX
PI   Forsberg G,  Erlandsson E,  Antonsson P,  Walse B;
XX
DR   WPI; 2003-201467/19.
XX
PT   Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT   receptor and four regions to determine binding to class II major
PT   histocompatibility complex, antibody to cancer associated cell surface
PT   structure.
XX
PS   Claim 12; Fig 10; 102pp; English.
XX
CC   The present sequence is a conjugate of a bacterial superantigen and an
CC   antibody moiety, and has been designed to target and destroy cancer
CC   cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
CC   was derived from staphylococcal enterotoxin E (SEE) by the incorporation
CC   of the following amino acid substitutions to reduce seroreactivity whilst
CC   maintaining production levels and biological activity: R20G, N21T, S24G,
CC   R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
CC   Fab moiety of the tumour reactive antibody 5T4. Substitutions were made
CC   in the 5T4 sequence to obtain higher yields: in the heavy chain, H41P,
CC   S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
CC   T77S, L78V and L83A. An expression vector comprising DNA encoding the
CC   conjugate can be used to transform host cells for recombinant production
CC   of the conjugate. The conjugate is useful for treating cancer, including
CC   cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
CC   cervix and prostate (claimed)
XX
SQ   Sequence 672 AA;

  Query Match             76.0%;  Score 972.5;  DB 6;  Length 672;
  Best Local Similarity   40.1%;  Pred. No. 2.1e-61;
  Matches  227;  Conservative    3;  Mismatches   13;  Indels  323;  Gaps    5;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSPGKGLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVS- 119
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||

Db         61 NQKFKDKATLTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQGTSVTVSS 120

Qy        120 ------------------------------------------------------------ 119

Db        121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180

Qy        120 -------------------------------------------SGG--------------- 122
                                                          |||
Db        181 LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEEINEKDLRKK 240

Qy        123 ------------------------------------------------------------ 122

Db        241 SELQGTALGNLKQIYYYNSKAITSSEKSADQFLTNTLLFKGFFTGHPWYNDLLVDLGSTA 300

Qy        123 ----------------GGSGGGGT--------GG------------------------- 132
                              |    |||        ||
Db        301 ATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQ 360

Qy        133 -------------------------------------GG------------------- 134
                                                    ||
Db        361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVS 420

Qy        135 -----------------------------------SSIVMTQTPTFLLVSAGDRVTIT 157
                                                  :|||||||| ||||||||||
Db        421 YDLFDAQGQYPDTLLRIYRDNTTISSTSLSISLYLYTTSIVMTQTPTSLLVSAGDRVTIT 480

Qy        158 CKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAED 217
              |||||||||||||||||||| |||||||||||||||| |||||||| |||::||||
Db        481 CKASQSVSNDVAWYQQKPGQSPKLLISYTSSRYAGVPDRFSGSGYGTDFTLTISSVQAED 540

Qy        218 LAVYFCQQDYNSPPTFGGGTKLEIKR 243
              |||||||||||||||||||||||||
Db        541 AAVYFCQQDYNSPPTFGGGTKLEIKR 566
```

```
RESULT 12
ADR70320
ID   ADR70320 standard; protein; 267 AA.
XX
AC   ADR70320;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Poliovirus receptor (PVR)-specific scFv2 protein.
XX
KW   poliovirus receptor; PVR; CD155; cluster of differentiation 155;
KW   receptor mediated adhesion modulation;
KW   cell trafficking behaviour modulation;
KW   cell invasion behaviour modulation; proliferative disorder; cancer;
KW   metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;
KW   scFv2.
XX
OS   Unidentified.
XX
PN   WO2004074324-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-EP001637.
XX
PR   24-FEB-2003; 2003US-0450064P.
PR   28-MAY-2003; 2003EP-00012314.
XX
PA   (XERI-) XERION PHARM AG.
PA   (TUFT ) UNIV TUFTS.
XX
PI   Unger CM,  Beste G,  Zehetmeier C,  Lain B,  Torella C,  Jay DG;
PI   Eustace BK,  Sloan KE;
XX
DR   WPI; 2004-652917/63.
DR   N-PSDB; ADR70322.
XX
PT   New molecules that modulate poliovirus receptor (PVR) mediated adhesion,
```

PT trafficking and/or invasion behavior of a cell expressing CD155 or PVR,
PT useful for preventing or treating proliferative disorders, such as
PT cancer.
XX
PS Claim 7; SEQ ID NO 4; 87pp; English.
XX
CC The invention comprises molecules that specifically bind to at least one
CC intra- or extracellular domain of the poliovirus receptor (PVR) - also
CC known as CD155 (cluster of differentiation 155). The molecules of the
CC invention have the ability to modulate receptor mediated adhesion,
CC trafficking and/or invasion behaviour of a cell expressing PVR. The
CC molecules of the invention are useful for the prevention and/or treatment
CC of proliferative disorders, cancer or metastasis. The molecules of the
CC invention are also useful for identifying agents that can modulate PVR-
CC mediated adhesion or invasion potential of cells. The present amino acid
CC sequence represents a PVR-specific scFv protein of the invention.
XX
SQ Sequence 267 AA;

Query Match 73.1%; Score 935; DB 8; Length 267;
Best Local Similarity 76.1%; Pred. No. 3.8e-59;
Matches 185; Conservative 19; Mismatches 31; Indels 8; Gaps 4;

```
Qy          3 QLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQ 62
              |||||||:||||||||||||| |||:|| | ||||||||||||||| |:|||| | |||
Db          1 QLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGIHPNNGDTSYNQ 60

Qy         63 KFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGG 122
              :|| || |||||||:|||||||||||||||||||| |       |||| |::|||:||
Db         61 RFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARWT----GDFDYWGQGTTLTVSTGG 116

Qy        123 GGSGGGGTGGGGSS--IVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||:|||||:  |||||:| |:  | ||||::||||||:|  :||||||||||||
Db        117 GGSGGGGSGGGGSALDIVMTQSPKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPK 176

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNS-PPTFGGGTKL 239
               ||   | ||:|||||| ||| ||||| ||| :|:|||| ||||| ||| | ||||||||
Db        177 ALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQ-YNSYPYTFGGGTKL 235

Qy        240 EIK 242
              |||
Db        236 EIK 238
```

RESULT 13
AAW90217
ID AAW90217 standard; protein; 580 AA.
XX
AC AAW90217;
XX
DT 10-MAY-1999 (first entry)
XX
DE Bispecific tetravalent antibody BiTAbB7-24-IG10H6.
XX
KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease; allergy;
KW therapy; human; bispecific tetravalent antibody; BiTAb;
KW BiTAbB7-24-1G10H6.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .24
FT		/note= "pelB signal peptide"
FT	Region	25. .138
FT		/note= "VH region anti B7.1 MAb"
FT	Peptide	139. .153
FT		/note= "(G4S3) flexible linker"
FT	Region	154. .262
FT		/note= "VL region anti B7.1 MAb"
FT	Misc-difference	261
FT		/note= "encoded by CTG"
FT	Region	263. .273
FT		/note= "human IgG3 hinge region"
FT	Domain	274. .308
FT		/note= "helix-turn-helix dimerisation domain"
FT	Domain	309. .319
FT		/note= "human IgG3 hinge domain"
FT	Region	320. .446
FT		/note= "VH region anti B7.2 MAb"
FT	Misc-difference	322. .327
FT		/note= "codons for these amino acids are not present in
FT		the DNA sequence for BTiTAbB7-24-1G1-H6 provided in the
FT		specification"
FT	Peptide	447. .461
FT		/note= "(G4S3)flexible linker"
FT	Region	462. .574
FT		/note= "VL region anti B7.2 MAb"
FT	Peptide	575. .580
FT		/note= "His6 tag"

XX
PN WO9858965-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-EP003791.
XX
PR 20-JUN-1997; 97EP-00870092.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Lorre K, Sablon E, Buyse M, Bosman A;
XX
DR WPI; 1999-105615/09.
DR N-PSDB; AAX01651.
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
PS Example 7.1; Fig 16; 182pp; English.
XX
CC This polypeptide comprises the bispecific tetravalent antibody BiTAbB7-24
CC -1G10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
CC anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2
CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
CC (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a
CC dimerisation domain (see AAW90219), which drives the homodimerisation of
CC the molecule. DNA (see AAX01651) encoding the BiTAb has been constructed
CC to allow expression of the BiTAb in transformed E. coli cells. The BiTAb
CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
CC and B7.2 that are expressed on the membrane of professional antigen-
CC presenting cells, leading to the inhibition of antigen- specific T cell
CC activation. The invention relates to such B7-binding molecules, methods
CC for their production, and their use for treating or preventing diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
SQ Sequence 580 AA;

Query Match 70.6%; Score 903.5; DB 2; Length 580;
Best Local Similarity 71.7%; Pred. No. 1.6e-56;
Matches 180; Conservative 27; Mismatches 35; Indels 9; Gaps 3;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||||||:| |||||||||||||||||||: |:|||||:|||||||| |:|  | | |
Db        325 QVQLQQSGPELEKPGASVKISCKASGYSFTGHNMNWVKQSNGKSLEWIGIIDPYYGGTSY 384

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN--YVMDYWGQVTSVTV 118
              | ||: || |||||||:||||:| |||||||||||||||     :  |:|||||| |:|||
Db        385 NPKPEGKATLTVDKSSSTAYMQLESLTSEDSAVYYCARFAYYGDYYYIMDYWGQGTTVTV 444

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV------SNDVAWYQ 172
```

```
           ||||||||||||:|||||  | :||:|:  | ||||: ||:|||:||||       | :||||
Db        445 SSGGGGSGGGGSGGGGSDIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNQKNYLAWYQ 504

Qy        173 QKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPT 232
           ||||||| ||| : |:| :|||||| ||| ||||: |||::||||||||:| | | |  |
Db        505 QKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFSLTISSVQAEDLAVYYCHQ-YLSSWT 563

Qy        233 FGGGTKLEIKR 243
           ||||||||||
Db        564 FGGGTKLEIKR 574
```

RESULT 14
AAW90218
ID AAW90218 standard; protein; 556 AA.
XX
AC AAW90218;
XX
DT 10-MAY-1999 (first entry)
XX
DE Bispecific tetravalent antibody BiTAb1G10-B7-24H6.
XX
KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW T cell activation; inhibitor; graft versus host disease;
KW transplant rejection; allograft rejection; autoimmune disease; allergy;
KW therapy; human; bispecific tetravalent antibody; BiTAb;
KW BiTAb1G10-B7-24H6.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .120
FT		/note= "VH region anti B7.2 MAb"
FT	Peptide	121. .135
FT		/note= "(G4S3) flexible linker"
FT	Region	136. .248
FT		/note= "VL region anti B7.2 MAb"
FT	Region	249. .259
FT		/note= "human IgG3 hinge region"
FT	Domain	260. .285
FT		/note= "helix-turn-helix dimerisation domain"
FT	Domain	286. .305
FT		/note= "human IgG3 hinge domain"
FT	Region	306. .426
FT		/note= "VH region anti B7.1 MAb"
FT	Peptide	427. .441
FT		/note= "(G4S3)flexible linker"
FT	Region	442. .550
FT		/note= "VL region anti B7.1 MAb"
FT	Peptide	551. .556
FT		/note= "His6 tag"

XX
PN WO9858965-A2.
XX
PD 30-DEC-1998.
XX
PF 22-JUN-1998; 98WO-EP003791.
XX
PR 20-JUN-1997; 97EP-00870092.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Lorre K, Sablon E, Buyse M, Bosman A;
XX
DR WPI; 1999-105615/09.
DR N-PSDB; AAX01652.
XX
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
PS Example 7.1; Fig 18; 182pp; English.
XX
CC This polypeptide comprises the bispecific tetravalent antibody BiTAb1G10-
CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
CC anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2
CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
CC (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a
CC dimerisation domain (see AAW90219), which drives the homodimerisation of
CC the molecule. DNA (see AAX01652) encoding the BiTAb has been constructed
CC to allow expression of the BiTAb in transformed E. coli cells. The BiTAb
CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
CC and B7.2 that are expressed on the membrane of professional antigen-
CC presenting cells, leading to the inhibition of antigen- specific T cell
CC activation. The invention relates to such B7-binding molecules, methods
CC for their production, and their use for treating or preventing diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)
XX
SQ Sequence 556 AA;

Query Match 70.2%; Score 897.5; DB 2; Length 556;
Best Local Similarity 71.9%; Pred. No. 4.2e-56;
Matches 179; Conservative 26; Mismatches 35; Indels 9; Gaps 3;

```
Qy          3 QLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQ 62
              |||||||:| |||||||||||||||||||: |:|||||:||||||| |:|  | | ||
Db          1 QLQQSGPELEKPGASVKISCKASGYSFTGHNMNWVKQSNGKSLEWIGIIDPYYGGTSYNP 60

Qy         63 KFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN--YVMDYWGQVTSVTVSS 120
              ||: || |||||||:||||:| |||||||||||||     :  |:|||||| |:|||||
Db         61 KFEGKATLTVDKSSSTAYMQLESLTSEDSAVYYCARFAYYGDYYYIMDYWGQGTTVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV------SNDVAWYQQK 174
              |||||||||:||||| | :||:|: | ||||: ||:|||:||||       | :||||||
Db        121 GGGGSGGGGSGGGGSDIELTQSPSSLAVSAGEEVTMTCKSSQSVLYSSNQKNYLAWYQQK 180

Qy        175 PGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFG 234
              ||||| ||| : |:| :|||||| ||| ||||: |||::||||||||:| | | |  |||
Db        181 PGQSPKLLIYWASTRESGVPDRFTGSGSGTDFSLTISSVQAEDLAVYYCHQ-YLSSWTFG 239

Qy        235 GGTKLEIKR 243
              |||||||||
Db        240 GGTKLEIKR 248
```

RESULT 15
ADG17481
ID ADG17481 standard; protein; 244 AA.
XX
AC ADG17481;
XX
DT 11-MAR-2004 (first entry)
XX
DE Anti-CD22 antibody related variant MLV 11.2 protein SEQ ID NO:6.
XX
KW anti-CD22 antibody; antibody; humanised anti-CD22 antibody;
KW immunoconjugate; malignant B cell growth inhibition; cytostatic;
KW lymphoma; B cell non-Hodgkin's lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003104425-A2.
XX
PD 18-DEC-2003.
XX
PF 09-JUN-2003; 2003WO-US018201.
XX
PR 07-JUN-2002; 2002US-0387306P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak S, Arndt M, Krauss J;

XX
DR WPI; 2004-062346/06.
DR N-PSDB; ADG17493.
XX
PT New anti-CD22 antibody having a VH domain and a VL domain comprising at
PT least two amino acid substitutions, useful in diagnosing or treating
PT lymphoma, e.g. B cell non-Hodgkin's lymphoma.
XX
PS Disclosure; SEQ ID NO 6; 66pp; English.
XX
CC The present invention describes a stable anti-CD22 antibody having a VH
CC domain and a VL domain, where the sequences of the VH and VL domains are
CC at least 70% or 90% identical to the a sequence of 244 amino acids
CC (ADG17476) and the antibody comprises at least two amino acid
CC substitutions with respect to ADG17476, Gln replacing Glu at position 6,
CC Val replacing Ser at position 12 or Lys replacing Asn at position 62 of
CC the VH domain. Also described: (1) an isolated nucleic acid encoding a
CC stable humanised anti-CD22 antibody described above and that has an LL2
CC binding specificity; (2) an immunoconjugate comprising a stable anti-CD22
CC antibody described above; (3) a nucleic acid encoding an immunoconjugate
CC of (1); (4) a method of inhibiting growth of a malignant B cell; and (5)
CC a method of detecting a cell that expresses CD22. The anti-CD22 antibody
CC has cytostatic activity. The antibodies are useful in diagnosing or
CC treating lymphoma, e.g. B cell non-Hodgkin's lymphoma. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 244 AA;

Query Match 69.5%; Score 889.5; DB 8; Length 244;
Best Local Similarity 69.9%; Pred. No. 6.3e-56;
Matches 174; Conservative 27; Mismatches 37; Indels 11; Gaps 3;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||||| :|||||||||:|||||||:|| |::||:||  |: ||||| ||| |  | |
Db          1 QVQLQQSGAELVKPGASVKMSCKASGYTFTSYWLHWIKQRPGQGLEWIGYINPRNDYTEY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |||||||| || ||||:||||:| |||||||||||||  : |     |||| |::||||
Db         61 NQKFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARRDITT----FYWGQGTTLTVSS 116

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV------SNDVAWYQQK 174
              |||||||||:||||| |||||:|: | ||||: ||::||:||||       | :||||||
Db        117 GGGGSGGGGSGGGGSDIVMTQSPSSLAVSAGENVTMSCKSSQSVLYSANHKNYLAWYQQK 176

Qy        175 PGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFG 234
              ||||| ||| : |:| :|||||| ||| ||||| ||| :| ||||:|:| | | |  |||
Db        177 PGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISRVQVEDLAIYYCHQ-YLSSWTFG 235

Qy        235 GGTKLEIKR 243
              |||||||||
Db        236 GGTKLEIKR 244
```

Search completed: March 11, 2005, 14:54:33
Job time : 76 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:50:22 ; Search time 22 Seconds
(without alignments)
824.533 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....QQDYNSPPTFGGGTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	883	69.0	288	3	US-09-423-439-38	Sequence 38, Appl
2	883	69.0	673	3	US-09-423-439-32	Sequence 32, Appl
3	861	67.3	249	2	US-08-797-689-18	Sequence 18, Appl
4	861	67.3	249	4	US-09-984-186-18	Sequence 18, Appl
5	858	67.1	267	4	US-09-419-788-30	Sequence 30, Appl
6	853	66.7	260	2	US-08-447-402-1	Sequence 1, Appli
7	848	66.3	269	3	US-09-070-408-132	Sequence 132, App
8	843.5	65.9	297	4	US-09-486-814A-2	Sequence 2, Appli
9	839.5	65.6	240	4	US-10-092-246-35	Sequence 35, Appl
10	838.5	65.6	240	4	US-10-096-246A-35	Sequence 35, Appl
11	833.5	65.2	240	4	US-10-092-246-36	Sequence 36, Appl
12	833.5	65.2	240	4	US-10-096-246A-37	Sequence 37, Appl
13	833.5	65.2	273	2	US-08-403-853-18	Sequence 18, Appl
14	831.5	65.0	240	4	US-10-092-246-37	Sequence 37, Appl
15	829	64.8	244	2	US-08-553-497A-20	Sequence 20, Appl
16	825.5	64.5	240	4	US-10-096-246A-36	Sequence 36, Appl
17	817	63.9	246	1	US-08-257-341-7	Sequence 7, Appli
18	817	63.9	246	2	US-08-553-497A-24	Sequence 24, Appl
19	817	63.9	252	1	US-08-133-804-4	Sequence 4, Appli
20	817	63.9	252	1	US-08-461-838-4	Sequence 4, Appli
21	817	63.9	252	2	US-08-461-386-4	Sequence 4, Appli
22	817	63.9	367	1	US-08-257-341-5	Sequence 5, Appli
23	814	63.6	244	2	US-08-553-497A-22	Sequence 22, Appl
24	813.5	63.6	239	3	US-08-279-772A-8	Sequence 8, Appli
25	813.5	63.6	239	3	US-08-902-486-11	Sequence 11, Appl
26	813.5	63.6	599	1	US-08-463-163-3	Sequence 3, Appli
27	813	63.6	353	4	US-09-203-958A-4	Sequence 4, Appli
28	810	63.3	355	3	US-08-875-811-57	Sequence 57, Appl
29	809.5	63.3	256	4	US-09-526-738A-2	Sequence 2, Appli
30	809.5	63.3	258	4	US-09-526-738A-4	Sequence 4, Appli
31	807.5	63.1	637	1	US-08-235-838-16	Sequence 16, Appl
32	807.5	63.1	637	2	US-08-465-473B-16	Sequence 16, Appl
33	805.5	63.0	240	2	US-08-800-198-8	Sequence 8, Appli
34	805.5	63.0	240	3	US-09-296-595-8	Sequence 8, Appli
35	805.5	63.0	530	4	US-08-840-713-2	Sequence 2, Appli
36	805.5	63.0	615	4	US-08-840-713-35	Sequence 35, Appl
37	805.5	63.0	617	4	US-08-840-713-37	Sequence 37, Appl
38	805.5	63.0	637	1	US-08-235-838-14	Sequence 14, Appl
39	805.5	63.0	637	2	US-08-465-473B-14	Sequence 14, Appl
40	805.5	63.0	711	1	US-08-235-838-7	Sequence 7, Appli
41	805.5	63.0	711	2	US-08-465-473B-7	Sequence 7, Appli
42	802.5	62.7	240	4	US-10-092-246-34	Sequence 34, Appl
43	802.5	62.7	241	1	US-08-235-838-11	Sequence 11, Appl
44	802.5	62.7	241	2	US-08-465-473B-11	Sequence 11, Appl
45	802	62.7	241	4	US-09-581-345-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match 69.0%; Score 883; DB 3; Length 288;
Best Local Similarity 67.6%; Pred. No. 5.4e-70;
Matches 169; Conservative 38; Mismatches 35; Indels 8; Gaps 3;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||| | :|||||||::|||||||:||||::|||||  |: ||||| :||: | : |
Db         23 QVQLQQPGAELVKPGASVQLSCKASGYTFTGYWIHWVKQRPGQGLEWIGEVNPSTGRSDY 82

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI-TNYVMDYWGQVTSVTVS 119
              |:|||:|| ||||||||||||:| ||||||||||||||      : |||||| |:||||
```

```
Db          83 NEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDDAMDYWGQGTTVTVS 142

Qy         120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND------VAWYQQ 173
               |||||||||:|||| | ::|:|: | ||||::||::||:||: |       :|||||
Db         143 SGGGGSGGGGSGGGGSDIELSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQ 202

Qy         174 KPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTF 233
               :|||| ||| : |:| :|||||| ||| ||||| |||::||||||:|:|:| | :  ||
Db         203 RPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISSVQAEDLAIYYCKQSY-TLRTF 261

Qy         234 GGGTKLEIKR 243
               ||||||||||
Db         262 GGGTKLEIKR 271


RESULT 2
US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
;   GENERAL INFORMATION:
;        APPLICANT: EMERY, Stephen Charles
;                   BLAKEY, David Charles
;        TITLE OF INVENTION: CHEMICAL COMPOUNDS
;        NUMBER OF SEQUENCES: 60
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pillsbury Winthrop, L.L.P.
;             STREET: 1100 New York Ave., N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/423,439
;             FILING DATE: 09-No. 6339070-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: PCT/GB98/01294
;             FILING DATE: 05-MAY-1998
;             APPLICATION NUMBER: GB 9709421.3
;             FILING DATE: 10-MAY-1997
;   INFORMATION FOR SEQ ID NO: 32:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 673 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

  Query Match             69.0%;  Score 883;  DB 3;  Length 673;
  Best Local Similarity   67.6%;  Pred. No. 1.6e-69;
  Matches  169;  Conservative   38;  Mismatches   35;  Indels    8;  Gaps    3;

Qy           1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
               :|||| | :|||||||::|||||||:||||::|||||  |: ||||| :||: | : |
Db          20 QVQLQQPGAELVKPGASVQLSCKASGYTFTGYWIHWVKQRPGQGLEWIGEVNPSTGRSDY 79

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI-TNYVMDYWGQVTSVTVS 119
               |:|||:|| |||||||||||||:| |||||||||||||      :  |||||| |:||||
Db          80 NEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDDAMDYWGQGTTVTVS 139

Qy         120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND------VAWYQQ 173
               |||||||||:|||| | ::|:|: | ||||::||::||:||: |       :|||||
Db         140 SGGGGSGGGGSGGGGSDIELSQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAWYQQ 199

Qy         174 KPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTF 233
               :|||| ||| : |:| :|||||| ||| ||||| |||::||||||:|:|:| | :  ||
Db         200 RPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISSVQAEDLAIYYCKQSY-TLRTF 258

Qy         234 GGGTKLEIKR 243
               ||||||||||
Db         259 GGGTKLEIKR 268


RESULT 3
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
;  GENERAL INFORMATION:
;    APPLICANT:  Fleer, Reinhard
;    APPLICANT:  Fournier, Alain
;    APPLICANT:  Guitton, Jean-Dominique
;    APPLICANT:  Jung, Gerard
;    APPLICANT:  Yeh, Patrice
;    TITLE OF INVENTION:  NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;    TITLE OF INVENTION:  PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;    TITLE OF INVENTION:  CONTAINING SAID POLYPEPTIDES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,689
;      FILING DATE:  31-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/256,927
;      FILING DATE:  28-JUL-1994
;      APPLICATION NUMBER:  FR 92/01064
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR93/00085
;      FILING DATE:  28-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith Ph.D., Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92006-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  249 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-797-689-18

  Query Match             67.3%;  Score 861;  DB 2;  Length 249;
  Best Local Similarity   67.9%;  Pred. No. 3.9e-68;
  Matches  167;  Conservative   28;  Mismatches   47;  Indels    4;  Gaps    1;

Qy           1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
               :|||:||||:||||||||||||||||:|:  :|:||||  |: |||||||| | :| | |
Db           4 QVQLEQSGPELVKPGASVKISCKASGYAFSRSWMNWVKQRPGQGLEWIGRIYPGDGDTKY 63

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN----YVMDYWGQVTSV 116
               | ||| || || |:||:||||:| ||||  ||||:||:     :    | |||||| |:|
Db          64 NGKFKGKATLTADRSSSTAYMQLSSLTSVGSAVYFCAKENNRFDERGYYAMDYWGQGTTV 123

Qy         117 TVSSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPG 176
```

```
                ||||||||||||||:|||||:| :||:|  :  | ||||:|||||||  |   |||||||||
Db        124 TVSSGGGGSGGGGSGGGGSNIQLTQSPNSMSTSVGDRVSITCKASQDVDTSVAWYQQKPG 183

Qy        177 QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGG 236
              ||| ||| : |:|: |||||| ||| ||||| ||| :|:|| | |||||  : | |||||
Db        184 QSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDSADYFCQQYSSYPWTFGGG 243

Qy        237 TKLEIK 242
              ||||||
Db        244 TKLEIK 249


RESULT 4
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686179
;  GENERAL INFORMATION:
;       APPLICANT: Fleer, Reinhard
;                  Fournier, Alain
;                  Guitton, Jean-Dominique
;                  Jung, Gerard
;                  Yeh, Patrice
;       TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;                           PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;                           CONTAINING SAID POLYPEPTIDES
;       NUMBER OF SEQUENCES: 36
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Rhone-Poulenc Rorer Inc.
;            STREET: 500 Arcola Road, 3C43
;            CITY: Collegeville
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 19426
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: Macintosh
;            OPERATING SYSTEM: System 7.1
;            SOFTWARE: Word 5.1 (PatentIn)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/984,186
;            FILING DATE: 29-Oct-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/797,689
;            FILING DATE: 31-JAN-1997
;            APPLICATION NUMBER: US 08/256,927
;            FILING DATE: 28-JUL-1994
;            APPLICATION NUMBER: FR 92/01064
;            FILING DATE: 31-JAN-1992
;            APPLICATION NUMBER: PCT/FR93/00085
;            FILING DATE: 28-JAN-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Smith Ph.D., Julie K.
;            REGISTRATION NUMBER: P-38,619
;            REFERENCE/DOCKET NUMBER: ST92006-US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (610) 454-3839
;            TELEFAX: (610) 454-3808
;  INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 249 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

  Query Match             67.3%;  Score 861;  DB 4;  Length 249;
  Best Local Similarity   67.9%;  Pred. No. 3.9e-68;
  Matches  167;  Conservative   28;  Mismatches   47;  Indels    4;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||:||||:|||||||||||||||||:|:  :|:||||  |: |||||| | :| | |

Db          4 QVQLEQSGPELVKPGASVKISCKASGYAFSRSWMNWVKQRPGQGLEWIGRIYPGDGDTKY 63

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN----YVMDYWGQVTSV 116
              | ||| || || |:||:||||:| |||| ||||:||:     :     | |||||| |:|
Db         64 NGKFKGKATLTADRSSSTAYMQLSSLTSVGSAVYFCAKENNRFDERGYYAMDYWGQGTTV 123

Qy        117 TVSSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPG 176
              |||||||||||||:|||||:| :||:|  :  | ||||:|||||| |   |||||||||
Db        124 TVSSGGGGSGGGGSGGGGSNIQLTQSPNSMSTSVGDRVSITCKASQDVDTSVAWYQQKPG 183

Qy        177 QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGG 236
              ||| ||| : |:|: |||||| ||| ||||| ||| :|:|| | |||||  : | |||||
Db        184 QSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDSADYFCQQYSSYPWTFGGG 243

Qy        237 TKLEIK 242
              ||||||
Db        244 TKLEIK 249


RESULT 5
US-09-419-788-30
; Sequence 30, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
;  APPLICANT: FISCHER, Rainer
;  APPLICANT: SCHILLBERG, Stefan
;  APPLICANT: NAHRING, Jorg
;  APPLICANT: SACK, Markus
;  APPLICANT: MONECKE, Michael
;  APPLICANT: LIAO, Yu-Cai
;  APPLICANT: SPIEGEL, Holger
;  APPLICANT: ZIMMERMAN, Sabine
;  APPLICANT: EMANS, Neil
;  TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
;  TITLE OF INVENTION: Resistance
;  FILE REFERENCE: 0147-0189P
;  CURRENT APPLICATION NUMBER: US/09/419,788
;  CURRENT FILING DATE: 1999-10-18
;  EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
;  EARLIER FILING DATE: 1998-10-16
;  EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
;  EARLIER FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 163
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
;   OTHER INFORMATION: natural origin
US-09-419-788-30

  Query Match             67.1%;  Score 858;  DB 4;  Length 267;
  Best Local Similarity   69.2%;  Pred. No. 7.9e-68;
  Matches  173;  Conservative   24;  Mismatches   43;  Indels   10;  Gaps    4;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||:||||| :|||||||||||||| |||||| |:||||||||||||| |||  | | |
Db          1 EVKLQQSGAELVKPGASVKISCKASDYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYV--MDYWGQVTSVTV 118
              ||||| || |||||||:||||:| |||||||||||||   :  |||    |||| | |||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCA---VGGNYVDWFAYWGQGTLVTV 117

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQ 173
              ||||||||||:||||| |::||:|  | || ||  :|:|::|||:  ||    : || |
Db        118 SSGGGGSGGGGSGGGGSDILLTQSPLSLPVSLGDHASISCRSSQSLVHSNGNTYLHWYLQ 177

Qy        174 KPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTF 233
              ||||| |||   |:|::|:|||| ||| ||||| || ::|||| |||| |  : | ||
Db        178 NPGQSPKLLIYKVSNRFSGIPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTF 237
```

```
Qy        234 GGGTKLEIKR 243
              |||||||:||
Db        238 GGGTKLELKR 247


RESULT 6
US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Brent
;    APPLICANT:  Georgiou, George
;    APPLICANT:  Chen, Gang
;    TITLE OF INVENTION:  IMMUNOASSAY AND ANTIBODY SELECTION
;    TITLE OF INVENTION:  METHODS USING CELL SURFACE EXPRESSED
;    TITLE OF INVENTION:  LIBRARIES
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P. O. Box 4433
;      CITY:  Houston
;      STATE:  TX
;      COUNTRY:  USA
;      ZIP:  77210-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,402
;      FILING DATE:  23-MAY-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/258,543
;      FILING DATE:  10-JUN-1994
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/794,731
;      FILING DATE:  15-NOV-1991
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTSB:584\KIT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  260 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-447-402-1

  Query Match             66.7%;  Score 853;  DB 2;  Length 260;
  Best Local Similarity   66.9%;  Pred. No. 2.1e-67;
  Matches  166;  Conservative   33;  Mismatches   43;  Indels    6;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||::|||:||| || :||:||:|||||||::|| |:| :||| |
Db          1 EVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |||||  || |||||||:||||||||||||||||||||| |:    : |||||   ||||||
Db         61 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSG-NKWAMDYWGHGASVTVSS 119

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQKP 175
              |||||||||:|||||  ||:||:|  | || | | ||:|::|||:  ||    : ||||||
Db        120 GGGGSGGGGSGGGGSDIVLTQSPASLAVSLGQRATISCRSSQSLVHSNGNTYLNWYQQKP 179

Qy        176 GQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGG 235
              || | |||   |:|::||| || |||  :||| ||  :: :| |:|:| |  : |||||
Db        180 GQPPKLLIYKVSNRFSGVPARFSGSGSESDFTLTIDPVEEDDAAIYYCSQTTHVPPTFGS 239

Qy        236 GTKLEIKR 243
              |||||:||
Db        240 GTKLELKR 247


RESULT 7
US-09-070-408-132
; Sequence 132, Application US/09070408
; Patent No. 6180341
;  GENERAL INFORMATION:
;    APPLICANT:  Iverson, Brent L.
;    APPLICANT:  Georgiou, George
;    APPLICANT:  Burks, Elizabeth A.
;    TITLE OF INVENTION:  IN VITRO SCANNING SATURATION MUTAGENESIS
;    TITLE OF INVENTION:  OF PROTEINS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/070,408
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/045,409
;      FILING DATE:  01-MAY-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMillian, Nabeela R.
;      REGISTRATION NUMBER:  P-43,363
;      REFERENCE/DOCKET NUMBER:  UTSB:593
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/447-7577
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  269 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-09-070-408-132

  Query Match             66.3%;  Score 848;  DB 3;  Length 269;
  Best Local Similarity   67.3%;  Pred. No. 6e-67;
  Matches  167;  Conservative   32;  Mismatches   43;  Indels    6;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||::|||:||| || :||:||:|||||||::|| |:| :||| |
Db          2 EVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGY 61

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |||||  || |||||||:|||||||||||||||||||||| |:    : |||||   ||||||
Db         62 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSG-NKWAMDYWGHGASVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQKP 175
              |||||||||:|||||  ||:||||  | || ||: ||:|::|||:  ||    : || ||
Db        121 GGGGSGGGGSGGGGSDIVLTQTPPSLPVSLGDQATISCRSSQSLVHSNGNTYLNWYLQKA 180

Qy        176 GQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGG 235
              |||| |||   |:|::||| || ||| |:||| ||  :: :| |:|:| |  : |||||
Db        181 GQSPKLLIYKVSNRFSGVPARFSGSGSGSDFTLTIDRVEEDDAAIYYCSQTTHVPPTFGS 240
```

```
Qy        236 GTKLEIKR 243
              |||||| |
Db        241 GTKLEIIR 248


RESULT 8
US-09-486-814A-2
; Sequence 2, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
;  APPLICANT: YAMAMOTO, Masato
;  APPLICANT:  HAYASHI, No. 6562599io
;  APPLICANT:  YAMAMOTO, Hiroko
;  APPLICANT:  TOHDOH, Naoki
;  TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
;  TITLE OF INVENTION:  PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
;  TITLE OF INVENTION:  HEPATITIS B CONTAINING THESE
;  FILE REFERENCE: 0020-4682P
;  CURRENT APPLICATION NUMBER: US/09/486,814A
;  CURRENT FILING DATE:  2002-06-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 297
;   TYPE: PRT
;   ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(145)
;   OTHER INFORMATION: Identification Method: P
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (177)..(279)
;   OTHER INFORMATION: Identification Method: P
US-09-486-814A-2

  Query Match             65.9%;  Score 843.5;  DB 4;  Length 297;
  Best Local Similarity   67.9%;  Pred. No. 1.7e-66;
  Matches  167;  Conservative   28;  Mismatches   42;  Indels    9;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:||:|||:| ||||||||||||||||||| | |||||:|||||||| | | || | |
Db         40 QVKLQESGPELEKPGASVKISCKASGYSFTGYNMKWVKQSNGKSLEWIGYIYPYNGGTGY 99

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| ||||||||||||||        :||||| |:|||||
Db        100 NQKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR------LGLDYWGQGTTVTVSS 153

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV-SNDVAWYQQKPGQSP 179
              |||||||||:||||| | :||:|| :  | |:::|||| || |: || : |||||||  ||
Db        154 GGGGSGGGGSGGGGSDIELTQSPTTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSP 213

Qy        180 TLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPP--TFGGGT 237
              |||  ||:  :|:| || ||| || :: || |::|||:| |:|||  : |   ||| ||
Db        214 KLLIYRTSNLASGIPARFSGSGSGTSYSLTIGTMEAEDVATYYCQQGSSIPRIFTFGAGT 273

Qy        238 KLEIKR 243
              ||||||
Db        274 KLEIKR 279


RESULT 9
US-10-092-246-35
; Sequence 35, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35

  Query Match             65.6%;  Score 839.5;  DB 4;  Length 240;
  Best Local Similarity   66.3%;  Pred. No. 2.9e-66;
  Matches  161;  Conservative   27;  Mismatches   50;  Indels    5;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||:|||:|||||||||||||||||:|| |::|||    |: |||||   |    | |
Db          3 QVQLQESGPELVKPGASVKISCKASGYTFTDYHVHWVKGKPGQGLEWIGMTYPGFDNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              :: || || |||| || | ||:| ||||||:|||:|||        :||||| |:|||||
Db         63 SETFKGKATLTVDTSSNTVYMQLSSLTSEDTAVYFCARGV-----GLDYWGQGTTVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:| |:: | |||: ||||||| |   | ||||:|||||
Db        118 GGGGSGGGGSGGGGSDIELTQSPKFVVTSIGDRIRITCKASQDVDTAVGWYQQRPGQSPK 177

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||| ::|:|: |||||| ||| ||||| |||  |:|||| ||| |  : | ||| |||||
Db        178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNAQSEDLADYFCHQYSSHPFTFGSGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 10
US-10-096-246A-35
; Sequence 35, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: mouse
US-10-096-246A-35

  Query Match             65.6%;  Score 838.5;  DB 4;  Length 240;
  Best Local Similarity   66.3%;  Pred. No. 3.6e-66;
  Matches  161;  Conservative   27;  Mismatches   50;  Indels    5;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||:|||:|||||||||||||||||:|| |::|||    |: |||||   |    | |
Db          3 QVQLQESGPELVKPGASVKISCKASGYTFTDYHVHWVKGKPGQGLEWIGMTYPGFDNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              :: || || |||| || | ||:| ||||||:|||:|||        :||||| |:|||||
Db         63 SETFKGKATLTVDTSSNTVYMQLSSLTSEDTAVYFCARGV-----GLDYWGQGTTVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:| |:: | |||: ||||||| |   | ||||:|||||
Db        118 GGGGSGGGGSGGGGSDIELTQSPKFVVTSIGDRIRITCKASQDVDTAVGWYQQRPGQSPK 177
```

```
Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||| ::|:|: |||||| ||| ||||| ||| |:|||| ||| |  : | ||| |||||
Db        178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNAQSEDLADYFCHQYSSYPFTFGSGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 11
US-10-092-246-36
; Sequence 36, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-36

  Query Match             65.2%;  Score 833.5;  DB 4;  Length 240;
  Best Local Similarity   66.3%;  Pred. No. 9.9e-66;
  Matches  161;  Conservative   26;  Mismatches   51;  Indels    5;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||:|||:||||||||||||||||:|| |::|||   |: |||||   |    | |
Db          3 QVQLQESGPELVKPGASVKISCKASGYTFTDYHVHWVKGKPGQGLEWIGMTYPGFDNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              :: || || |||| || | ||:| ||||||:|||:|||        :||||| |:|||||
Db         63 SETFKGKATLTVDTSSNTVYMQLSSLTSEDTAVYFCARGV-----GLDYWGQGTTVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:|  |   | |||: ||||||| |    | ||||:|||||
Db        118 GGGGSGGGGSGGGGSDIELTQSPNSLSTSIGDRIRITCKASQDVDTAVGWYQQRPGQSPK 177

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||| ::|:|: |||||| ||| ||||| ||| :|:|||| ||| |  : | ||| |||||
Db        178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 12
US-10-096-246A-37
; Sequence 37, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: mouse
US-10-096-246A-37

  Query Match             65.2%;  Score 833.5;  DB 4;  Length 240;
  Best Local Similarity   66.3%;  Pred. No. 9.9e-66;
  Matches  161;  Conservative   26;  Mismatches   51;  Indels    5;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||:|||:||||||||||||||||:|| |::|||   |: |||||   |    | |
Db          3 QVQLQESGPELVKPGASVKISCKASGYTFTDYHVHWVKGKPGQGLEWIGMTYPGFDNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              :: || || |||| || | ||:| ||||||:|||:|||        :||||| |:|||||
Db         63 SETFKGKATLTVDTSSNTVYMQLSSLTSEDTAVYFCARGV-----GLDYWGQGTTVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:|  |   | |||: ||||||| |    | ||||:|||||
Db        118 GGGGSGGGGSGGGGSDIELTQSPNSLSTSIGDRIRITCKASQDVDTAVGWYQQRPGQSPK 177

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||| ::|:|: |||||| ||| ||||| ||| :|:|||| ||| |  : | ||| |||||
Db        178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 13
US-08-403-853-18
; Sequence 18, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
;    APPLICANT:  HUDSON, Peter J.
;    APPLICANT:  LAH, Maria
;    APPLICANT:  KORRT, Alex A.
;    APPLICANT:  IRVING, Robert A.
;    APPLICANT:  ATWELL, John L.
;    APPLICANT:  MALBY, Robyn L.
;    APPLICANT:  POWER, Barbara E.
;    APPLICANT:  COLMAN, Peter M.
;    TITLE OF INVENTION:  TARGET BINDING POLYPEPTIDE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,853
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/AU93/00491
;      FILING DATE:  24-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PL 4973
;      FILING DATE:  25-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16786/189/CHAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
```

```
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-403-853-18

  Query Match             65.2%;  Score 833.5;  DB 2;  Length 273;
  Best Local Similarity   67.2%;  Pred. No. 1.2e-65;
  Matches  164;  Conservative   26;  Mismatches   51;  Indels    3;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||| :|||||||::|||||||:|| | |:||||| |: |||||    | || | |
Db         23 QVQLQQSGAELVKPGASVRMSCKASGYTFTNYNMYWVKQSPGQGLEWIGIFYPGNGDTSY 82

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY--VMDYWGQVTSVTV 118
              |||||||| || |||| ||||:| |||||||||||||||     |    |||||  |:|||
Db         83 NQKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYYCARSGGSYRYDGGFDYWGQGTTVTV 142

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||  | :||| : |   | ||||||:|:||| :|| : |||| |   :
Db        143 -SGGGGSGGGGSGGGGSDIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGT 201

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                ||| |||: :: || || ||| |||:: ||| |: ||:| ||||||:  | |||||||
Db        202 VKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPPTFGGGTK 261

Qy        239 LEIK 242
              |||:
Db        262 LEIR 265


RESULT 14
US-10-092-246-37
; Sequence 37, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37

  Query Match             65.0%;  Score 831.5;  DB 4;  Length 240;
  Best Local Similarity   65.8%;  Pred. No. 1.5e-65;
  Matches  160;  Conservative   27;  Mismatches   51;  Indels    5;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||:|||:|||||||||||||||||:|| |::||||   |: |||||   |    | |
Db          3 QVQLQESGPELVKPGASVKISCKASGYTFTDYHVHWVKGKPGQGLEWIGMTYPGFDNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              :: || || |||| || | ||:| ||||||:|||:|||        :|||||  |:|||||
Db         63 SETFKGKATLTVDTSSNTVYMQLSSLTSEDTAVYFCARGV-----GLDYWGQGTTVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:|||||  ::||:|  |  | |||: |||||| |   | ||||:|||||
Db        118 GGGGSGGGGSGGGGSDEILTQSPNSLSTSIGDRIRITCKASQDVDTAVGWYQQRPGQSPK 177

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||| ::|:|: |||||| ||| ||||| ||| :|:|||| ||| |  : | ||| |||||
Db        178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCHQYSSYPFTFGSGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 15
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  244 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-20

  Query Match             64.8%;  Score 829;  DB 2;  Length 244;
  Best Local Similarity   66.9%;  Pred. No. 2.5e-65;
  Matches  164;  Conservative   27;  Mismatches   50;  Indels    4;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||| :|||||||||:|||||||:|| ::||||||  |: |||||  ||:|| | |
Db          1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSHWMHWVKQRAGQGLEWIGEFNPSNGRTNY 60
```

```
Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCA-RSTMITNYVMDYWGQVTSVTVS 119
               |:||| || |||||||:||||:| |||||||||||| |          ||||| |:||||
Db          61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASRDYDYDGRYFDYWGQGTTVTVS 120

Qy         120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSP 179
               |||||||||||:||||| | :||:|  :  | |::||:|| || |||  : ||||||| ||
Db         121 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVSY-MYWYQQKPGSSP 179

Qy         180 TLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPP--TFGGGT 237
                |||  ||:  :||| || ||| || :: ||| ::||| | |:|||  : ||  ||||||
Db         180 RLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPMYTFGGGT 239

Qy         238 KLEIK 242
               |||||
Db         240 KLEIK 244
```

Search completed: March 11, 2005, 14:56:32
Job time : 24 secs

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:55:53 ; Search time 137 Seconds
(without alignments)
585.053 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....QQDYNSPPTFGGGTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1279	100.0	243	16	US-10-334-235-37	Sequence 37, Appl
2	1279	100.0	600	16	US-10-334-235-38	Sequence 38, Appl
3	1274	99.6	488	16	US-10-334-235-39	Sequence 39, Appl
4	994	77.7	243	17	US-10-879-994-10	Sequence 10, Appl
5	972.5	76.0	672	10	US-09-900-766-1	Sequence 1, Appli
6	909	71.1	331	14	US-10-059-261-169	Sequence 169, App
7	879	68.7	895	16	US-10-296-085A-19	Sequence 19, Appl
8	879	68.7	895	16	US-10-296-085A-20	Sequence 20, Appl
9	879	68.7	895	16	US-10-296-085A-27	Sequence 27, Appl
10	879	68.7	895	17	US-10-496-179-4	Sequence 4, Appli
11	879	68.7	896	16	US-10-296-085A-17	Sequence 17, Appl
12	879	68.7	896	16	US-10-296-085A-18	Sequence 18, Appl
13	879	68.7	896	16	US-10-296-085A-26	Sequence 26, Appl
14	879	68.7	896	17	US-10-496-179-2	Sequence 2, Appli
15	879	68.7	896	17	US-10-496-179-3	Sequence 3, Appli
16	879	68.7	896	17	US-10-496-179-7	Sequence 7, Appli
17	879	68.7	899	16	US-10-296-085A-28	Sequence 28, Appl
18	879	68.7	899	17	US-10-496-179-5	Sequence 5, Appli
19	870	68.0	631	15	US-10-120-198B-2	Sequence 2, Appli
20	869.5	68.0	264	14	US-10-114-716A-46	Sequence 46, Appl
21	861	67.3	249	9	US-09-984-186-18	Sequence 18, Appl
22	861	67.3	249	14	US-10-237-667-18	Sequence 18, Appl
23	861	67.3	249	14	US-10-237-708-18	Sequence 18, Appl
24	861	67.3	249	14	US-10-237-866-18	Sequence 18, Appl
25	861	67.3	249	14	US-10-237-871-18	Sequence 18, Appl
26	861	67.3	249	14	US-10-237-624-18	Sequence 18, Appl
27	861	67.3	249	15	US-10-702-536-18	Sequence 18, Appl
28	861	67.3	249	15	US-10-702-636-18	Sequence 18, Appl
29	853	66.7	260	10	US-09-782-672-2	Sequence 2, Appli
30	853	66.7	260	10	US-09-782-671B-2	Sequence 2, Appli
31	853	66.7	260	11	US-09-813-444-2	Sequence 2, Appli
32	841	65.8	258	15	US-10-239-656-59	Sequence 59, Appl
33	839.5	65.6	240	14	US-10-096-246-35	Sequence 35, Appl
34	833.5	65.2	240	14	US-10-096-246-36	Sequence 36, Appl
35	833.5	65.2	622	15	US-10-378-832A-2	Sequence 2, Appli
36	832	65.1	249	10	US-09-880-748-1635	Sequence 1635, Ap
37	832	65.1	249	15	US-10-293-418-1635	Sequence 1635, Ap
38	831.5	65.0	240	14	US-10-096-246-37	Sequence 37, Appl
39	830.5	64.9	242	14	US-10-259-087A-20	Sequence 20, Appl
40	830.5	64.9	242	16	US-10-689-006-20	Sequence 20, Appl
41	830.5	64.9	248	17	US-10-879-994-14	Sequence 14, Appl
42	829.5	64.9	248	10	US-09-880-748-1104	Sequence 1104, Ap
43	829.5	64.9	248	15	US-10-293-418-1104	Sequence 1104, Ap
44	825	64.5	245	14	US-10-138-505-40	Sequence 40, Appl
45	825	64.5	245	15	US-10-257-864A-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-10-334-235-37
; Sequence 37, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature secreted protein of 5T4 scFv, designated
; OTHER INFORMATION: 5T4scFv.1
US-10-334-235-37

Query Match 100.0%; Score 1279; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e-89;

```
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240

Qy        241 IKR 243
              |||
Db        241 IKR 243


RESULT 2
US-10-334-235-38
; Sequence 38, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide of 5T4Sab1
US-10-334-235-38

  Query Match           100.0%;  Score 1279;  DB 16;  Length 600;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-89;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 82

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 142

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 202

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 262

Qy        241 IKR 243
              |||
Db        263 IKR 265


RESULT 3
US-10-334-235-39
; Sequence 39, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
;   LENGTH: 488
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: peptide of B7-1.5T4.1
US-10-334-235-39

  Query Match           99.6%;  Score 1274;  DB 16;  Length 488;
  Best Local Similarity  100.0%;  Pred. No. 5.5e-89;
  Matches  242;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 306

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 366

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 486

Qy        241 IK 242
              ||
Db        487 IK 488


RESULT 4
US-10-879-994-10
; Sequence 10, Application US/10879994
; Publication No. US20050032175A1
; GENERAL INFORMATION:
;  APPLICANT: Stahl, Neil
;  APPLICANT:  Yancopoulos, George D.
```

```
;  APPLICANT:  Karow, Margaret
;  APPLICANT:  Smith, Eric
;  TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: REG 203E2
;  CURRENT APPLICATION NUMBER: US/10/879,994
;  CURRENT FILING DATE:  2004-06-29
;  PRIOR APPLICATION NUMBER: 10/610,452
;  PRIOR FILING DATE: 2003-06-30
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: mus musculus
US-10-879-994-10

  Query Match             77.7%;  Score 994;  DB 17;  Length 243;
  Best Local Similarity   78.7%;  Pred. No. 5.7e-68;
  Matches  192;  Conservative   19;  Mismatches   31;  Indels    2;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||| :| |||||||:|||||||:|| |:|||:||  |: ||||| |||: | : :
Db          1 QVQLQQSGAELAKPGASVKMSCKASGYTFTTYWMHWIKQRPGQGLEWIGYINPSTGYSEF 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |||| ||| || |:||:||||:| ||||||||||||||     ||  ||||| |::||||
Db         61 NQKFNDKATLTADRSSSTAYMQLNSLTSEDSAVYYCARDAYYGNY-EDYWGQGTTLTVSS 119

Qy        121 -GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSP 179
               |||||||||:|||||||||||||| ||||||||||||||||||| ||||||||||||
Db        120 AGGGGSGGGGSGGGGSSIVMTQTPKFLLVSAGDRVTITCKASQSVSYDVAWYQQKPGQSP 179

Qy        180 TLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKL 239
              ||| | |:||:|||||| ||| ||||||||||:|||||||||||| | || ||||||||
Db        180 KLLIYYESNRYSGVPDRFTGSGNGTDFTFTISTVQAEDLAVYFCQQVYTSPYTFGGGTKL 239

Qy        240 EIKR 243
              ||||
Db        240 EIKR 243


RESULT 5
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
;  APPLICANT: FORSBERG, GORAN
;  APPLICANT:  ERLANDSSON, EVA
;  APPLICANT:  ANTONSSON, PER
;  APPLICANT:  WALSE, BJORN
;  TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
;  FILE REFERENCE: P02188US0;10104199
;  CURRENT APPLICATION NUMBER: US/09/900,766
;  CURRENT FILING DATE:  2001-07-06
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 672
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(672)
;   OTHER INFORMATION: Conjugate protein
US-09-900-766-1

  Query Match             76.0%;  Score 972.5;  DB 10;  Length 672;
  Best Local Similarity   40.1%;  Pred. No. 7.2e-66;
  Matches  227;  Conservative    3;  Mismatches   13;  Indels  323;  Gaps    5;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||

Db          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSPGKGLEWIGRINPNNGVTLY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVS- 119
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 NQKFKDKATLTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQGTSVTVSS 120

Qy        120 ------------------------------------------------------------ 119

Db        121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180

Qy        120 ----------------------------------------SGG---------------- 122
                                                       |||
Db        181 LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEEINEKDLRKK 240

Qy        123 ------------------------------------------------------------ 122

Db        241 SELQGTALGNLKQIYYYNSKAITSSEKSADQFLTNTLLFKGFFTGHPWYNDLLVDLGSTA 300

Qy        123 ----------------GGSGGGGT--------GG------------------------- 132
                              |    |||        ||
Db        301 ATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQ 360

Qy        133 ----------------------------------------GG----------------- 134
                                                       ||
Db        361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVS 420

Qy        135 ----------------------------------SSIVMTQTPTFLLVSAGDRVTIT 157
                                               :|||||||| ||||||||||||
Db        421 YDLFDAQGQYPDTLLRIYRDNTTISSTSLSISLYLYTTSIVMTQTPTSLLVSAGDRVTIT 480

Qy        158 CKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAED 217
              |||||||||||||||||||| |||||||||||||||| ||||||||| |||::||||
Db        481 CKASQSVSNDVAWYQQKPGQSPKLLISYTSSRYAGVPDRFSGSGYGTDFTLTISSVQAED 540

Qy        218 LAVYFCQQDYNSPPTFGGGTKLEIKR 243
              |||||||||||||||||||||||||
Db        541 AAVYFCQQDYNSPPTFGGGTKLEIKR 566


RESULT 6
US-10-059-261-169
; Sequence 169, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
;  APPLICANT: EDELMAN, LENA
;  APPLICANT:  JACOTOT, ETIENNE DANIEL FRANCOIS
;  APPLICANT:  BRIAND, JEAN-PAUL
;  TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
;  TITLE OF INVENTION:  SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
;  TITLE OF INVENTION:  FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
;  TITLE OF INVENTION:  (PTPC)
;  FILE REFERENCE: 03495.0216
;  CURRENT APPLICATION NUMBER: US/10/059,261
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/265,594
;  PRIOR FILING DATE: 2001-02-02
;  NUMBER OF SEQ ID NOS: 325
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
;   LENGTH: 331
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv350
;   OTHER INFORMATION: peptide sequence
US-10-059-261-169

  Query Match             71.1%;  Score 909;  DB 14;  Length 331;
  Best Local Similarity   70.4%;  Pred. No. 2.3e-61;
  Matches  171;  Conservative   28;  Mismatches   42;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||| :| |||||||:||||||::|| |:||||||  |: ||||| || ::|   |
```

```
Db          86 QVQLQQSGAELAKPGASVKLSCKASGHTFTSYWMHWVKQRPGQGLEWIGYINLSSGYIKY 145

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
               ||:||||| || |||| |||| | ||| ||||||||||:   | :  ||||| |::||||
Db         146 NQEFKDKATLTADKSSNTAYMHLSSLTYEDSAVYYCARAAQATTF--DYWGQGTTLTVSS 203

Qy         121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
               |||||||||:||||| ||| |:  |:  | ||||:||||||| ||  | ||||||||||
Db         204 GGGGSGGGGSGGGGSDIVMIQSHKFMSTSVGDRVSITCKASQDVSTAVGWYQQKPGQSPK 263

Qy         181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
               ||| : |:|: ||||||  ||| |||:|  |||::||||||:|:||| |::||||||||||
Db         264 LLIYWASTRHTGVPDRFTGSGSGTDYTLTISSVQAEDLALYYCQQHYSTPPTFGGGTKLG 323

Qy         241 IKR 243
               |||
Db         324 IKR 326
```

RESULT 7
US-10-296-085A-19
; Sequence 19, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; TITLE OF INVENTION: FOR EXPRESSION THEREOF
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296,085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/573,797
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/380,484
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/389,565
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US98/04303
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/739,703
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/039,987
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/008,104
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-19

Query Match 68.7%; Score 879; DB 16; Length 895;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

```
Qy           1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
               |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db         515 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 574

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
               |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db         575 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 634
```

```
Qy         119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
               |||||||||||:||||| | |||| : |  | ||||||:|:||| : | : ||||||  :
Db         635 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 694

Qy         179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                  ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
Db         695 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 754

Qy         239 LEIK 242
               ||||
Db         755 LEIK 758
```

RESULT 8
US-10-296-085A-20
; Sequence 20, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
; APPLICANT: DAVID M. NEVILLE
; APPLICANT: JERRY T. THOMPSON
; APPLICANT: JUNG-HEE WOO
; APPLICANT: HUAIZHONG HU
; APPLICANT: SHENGLIN MA
; APPLICANT: JONATHAN MARK HEXHAM
; APPLICANT: MARY ELLEN DIGAN
; TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
; TITLE OF INVENTION: FOR EXPRESSION THEREOF
; FILE REFERENCE: 14028.0294U2
; CURRENT APPLICATION NUMBER: US/10/296,085A
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/573,797
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/380,484
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/389,565
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/US98/04303
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/739,703
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/039,987
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: 60/008,104
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: synthetic construct
US-10-296-085A-20

Query Match 68.7%; Score 879; DB 16; Length 895;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46; Indels 2; Gaps 1;

```
Qy           1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
               |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db         515 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 574

Qy          61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
               |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db         575 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 634

Qy         119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
               |||||||||||:||||| | |||| : |  | ||||||:|:||| : | : ||||||  :
Db         635 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 694

Qy         179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                  ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
```

```
Db        695 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 754

Qy        239 LEIK 242
              ||||
Db        755 LEIK 758


RESULT 9
US-10-296-085A-27
; Sequence 27, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
;  APPLICANT: DAVID M. NEVILLE
;  APPLICANT:  JERRY T. THOMPSON
;  APPLICANT:  JUNG-HEE WOO
;  APPLICANT:  HUAIZHONG HU
;  APPLICANT:  SHENGLIN MA
;  APPLICANT:  JONATHAN MARK HEXHAM
;  APPLICANT:  MARY ELLEN DIGAN
;  TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
;  TITLE OF INVENTION:  FOR EXPRESSION THEREOF
;  FILE REFERENCE: 14028.0294U2
;  CURRENT APPLICATION NUMBER: US/10/296,085A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/573,797
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 09/380,484
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: 09/389,565
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: PCT/US98/04303
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: 08/739,703
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/039,987
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: 60/008,104
;  PRIOR FILING DATE: 1995-10-30
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 895
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: synthetic construct
US-10-296-085A-27

  Query Match             68.7%;  Score 879;  DB 16;  Length 895;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        515 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 574

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db        575 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 634

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||  | ||||  :  |  |||||||:|:||| : | : ||||||  :
Db        635 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 694

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                 ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
Db        695 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 754

Qy        239 LEIK 242
              ||||
Db        755 LEIK 758


RESULT 10
US-10-496-179-4
; Sequence 4, Application US/10496179
; Publication No. US20050033034A1
; GENERAL INFORMATION:
;  APPLICANT: Novartis AG
;  APPLICANT:  Engel, Guenter
;  TITLE OF INVENTION: New combination
;  FILE REFERENCE: TX/4-32202A
;  CURRENT APPLICATION NUMBER: US/10/496,179
;  CURRENT FILING DATE:  2004-05-20
;  PRIOR APPLICATION NUMBER: GB 0128509.7
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: GB 0128510.5
;  PRIOR FILING DATE: 2001-11-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 895
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(895)
;   OTHER INFORMATION: synthetic construct
US-10-496-179-4

  Query Match             68.7%;  Score 879;  DB 17;  Length 895;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        515 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 574

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db        575 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 634

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||  | ||||  :  |  |||||||:|:||| : | : ||||||  :
Db        635 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 694

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                 ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
Db        695 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 754

Qy        239 LEIK 242
              ||||
Db        755 LEIK 758


RESULT 11
US-10-296-085A-17
; Sequence 17, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
;  APPLICANT: DAVID M. NEVILLE
;  APPLICANT:  JERRY T. THOMPSON
;  APPLICANT:  JUNG-HEE WOO
;  APPLICANT:  HUAIZHONG HU
;  APPLICANT:  SHENGLIN MA
;  APPLICANT:  JONATHAN MARK HEXHAM
;  APPLICANT:  MARY ELLEN DIGAN
;  TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
;  TITLE OF INVENTION:  FOR EXPRESSION THEREOF
;  FILE REFERENCE: 14028.0294U2
;  CURRENT APPLICATION NUMBER: US/10/296,085A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/573,797
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 09/380,484
```

```
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: 09/389,565
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: PCT/US98/04303
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: 08/739,703
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/039,987
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: 60/008,104
;  PRIOR FILING DATE: 1995-10-30
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 896
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: synthetic construct
US-10-296-085A-17

  Query Match             68.7%;  Score 879;  DB 16;  Length 896;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 575

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              ||||||| |||||||:|||||| ||||||||||||||||     :::  | ||  |:|||
Db        576 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 635

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||  | |||| : |  | ||||||:|:||| : | : ||||||  :
Db        636 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 695

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
Db        696 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 755

Qy        239 LEIK 242
              ||||
Db        756 LEIK 759


RESULT 12
US-10-296-085A-18
; Sequence 18, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
;  APPLICANT: DAVID M. NEVILLE
;  APPLICANT:  JERRY T. THOMPSON
;  APPLICANT:  JUNG-HEE WOO
;  APPLICANT:  HUAIZHONG HU
;  APPLICANT:  SHENGLIN MA
;  APPLICANT:  JONATHAN MARK HEXHAM
;  APPLICANT:  MARY ELLEN DIGAN
;  TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
;  TITLE OF INVENTION:  FOR EXPRESSION THEREOF
;  FILE REFERENCE: 14028.0294U2
;  CURRENT APPLICATION NUMBER: US/10/296,085A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/573,797
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 09/380,484
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: 09/389,565
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: PCT/US98/04303
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: 08/739,703
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/039,987
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: 60/008,104
;  PRIOR FILING DATE: 1995-10-30
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 896
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: synthetic construct
US-10-296-085A-18

  Query Match             68.7%;  Score 879;  DB 16;  Length 896;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 575

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              ||||||| |||||||:|||||| ||||||||||||||||     :::  | ||  |:|||
Db        576 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 635

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||  | |||| : |  | ||||||:|:||| : | : ||||||  :
Db        636 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 695

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||    | || ||||
Db        696 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 755

Qy        239 LEIK 242
              ||||
Db        756 LEIK 759


RESULT 13
US-10-296-085A-26
; Sequence 26, Application US/10296085A
; Publication No. US20040127682A1
; GENERAL INFORMATION:
;  APPLICANT: DAVID M. NEVILLE
;  APPLICANT:  JERRY T. THOMPSON
;  APPLICANT:  JUNG-HEE WOO
;  APPLICANT:  HUAIZHONG HU
;  APPLICANT:  SHENGLIN MA
;  APPLICANT:  JONATHAN MARK HEXHAM
;  APPLICANT:  MARY ELLEN DIGAN
;  TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
;  TITLE OF INVENTION:  FOR EXPRESSION THEREOF
;  FILE REFERENCE: 14028.0294U2
;  CURRENT APPLICATION NUMBER: US/10/296,085A
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/573,797
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: 09/380,484
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: 09/389,565
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: PCT/US98/04303
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: 08/739,703
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/039,987
;  PRIOR FILING DATE: 1997-03-05
;  PRIOR APPLICATION NUMBER: 60/008,104
;  PRIOR FILING DATE: 1995-10-30
;  NUMBER OF SEQ ID NOS: 122
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 896
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/Note =
;   OTHER INFORMATION: synthetic construct
US-10-296-085A-26

  Query Match             68.7%;  Score 879;  DB 16;  Length 896;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 575

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db        576 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 635

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||| | |||| : |  | ||||||:|:||| : | : ||||||  :
Db        636 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 695

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                 ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||     | || ||||
Db        696 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 755

Qy        239 LEIK 242
              ||||
Db        756 LEIK 759


RESULT 14
US-10-496-179-2
; Sequence 2, Application US/10496179
; Publication No. US20050033034A1
; GENERAL INFORMATION:
;  APPLICANT: Novartis AG
;  APPLICANT:  Engel, Guenter
;  TITLE OF INVENTION: New combination
;  FILE REFERENCE: TX/4-32202A
;  CURRENT APPLICATION NUMBER: US/10/496,179
;  CURRENT FILING DATE:  2004-05-20
;  PRIOR APPLICATION NUMBER: GB 0128509.7
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: GB 0128510.5
;  PRIOR FILING DATE: 2001-11-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 896
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(896)
;   OTHER INFORMATION: synthetic construct
US-10-496-179-2

  Query Match             68.7%;  Score 879;  DB 17;  Length 896;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 575

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db        576 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 635

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||| | |||| : |  | ||||||:|:||| : | : ||||||  :
Db        636 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 695

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                 ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||     | || ||||
Db        696 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 755

Qy        239 LEIK 242
              ||||
Db        756 LEIK 759


RESULT 15
US-10-496-179-3
; Sequence 3, Application US/10496179
; Publication No. US20050033034A1
; GENERAL INFORMATION:
;  APPLICANT: Novartis AG
;  APPLICANT:  Engel, Guenter
;  TITLE OF INVENTION: New combination
;  FILE REFERENCE: TX/4-32202A
;  CURRENT APPLICATION NUMBER: US/10/496,179
;  CURRENT FILING DATE:  2004-05-20
;  PRIOR APPLICATION NUMBER: GB 0128509.7
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: GB 0128510.5
;  PRIOR FILING DATE: 2001-11-28
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 896
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(896)
;   OTHER INFORMATION: synthetic construct
US-10-496-179-3

  Query Match             68.7%;  Score 879;  DB 17;  Length 896;
  Best Local Similarity   70.1%;  Pred. No. 1.3e-58;
  Matches  171;  Conservative   25;  Mismatches   46;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||:|||||||||||||| |:||||||||:|||:| |||  ||: |
Db        516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWMGLINPYKGVSTY 575

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
              |||||||| |||||||:|||||| |||||||||||||||     :::  | ||  |:|||
Db        576 NQKFKDKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTV 635

Qy        119 SSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
              ||||||||||:|||||| | |||| : |  | ||||||:|:||| : | : ||||||  :
Db        636 SSGGGGSGGGGSGGGGSDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT 695

Qy        179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                 ||| |||  ::||| :| ||| |||:: ||| |: ||:| |||||     | || ||||
Db        696 VKLLIYYTSRLHSGVPSKFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTK 755

Qy        239 LEIK 242
              ||||
Db        756 LEIK 759


Search completed: March 11, 2005, 15:07:46
Job time : 139 secs
```

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:49:22 ; Search time 16 Seconds
(without alignments)
1461.292 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....QQDYNSPPTFGGGTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	731.5	57.2	268	2	A56446	Ig heavy chain V r
2	710	55.5	249	2	S41374	single chain Fv an
3	646	50.5	233	2	JC5322	p53 specific singl
4	516	40.3	120	2	A49982	Ig heavy chain V r
5	502	39.2	128	2	I37267	Ig heavy chain V r
6	501	39.2	135	2	PS0057	Ig heavy chain pre
7	498	38.9	139	2	A27609	Ig heavy chain pre
8	496.5	38.8	225	2	S37484	Ig kappa chain - m
9	494	38.6	128	2	C37267	Ig heavy chain V r
10	483.5	37.8	151	2	PL0011	Ig heavy chain pre
11	481.5	37.6	144	2	B30502	Ig heavy chain V r
12	481	37.6	114	2	S26319	Ig heavy chain V r
13	480.5	37.6	117	1	MHMS4E	Ig heavy chain V r
14	480.5	37.6	140	2	T01407	Ig heavy chain (my
15	479.5	37.5	117	1	MHMSJ5	Ig heavy chain V r
16	479	37.5	118	1	MHMS38	Ig heavy chain V r
17	478.5	37.4	125	2	PH0100	Ig heavy chain V r
18	478	37.4	112	2	S09957	Ig heavy chain V-D
19	476	37.2	122	2	E37267	Ig heavy chain V r
20	476	37.2	137	2	H32513	Ig heavy chain pre
21	475	37.1	122	2	PH0887	Ig heavy chain V r
22	474	37.1	119	2	F30502	Ig heavy chain V r
23	472	36.9	128	2	A37267	Ig heavy chain V r
24	471.5	36.9	119	2	B53285	Ig heavy chain V a
25	471	36.8	107	2	S26320	Ig heavy chain V r
26	465	36.4	113	2	S55535	Ig heavy chain V r
27	465	36.4	120	2	F45722	anti-glycoprotein
28	465	36.4	127	2	S04577	Ig kappa chain pre
29	464	36.3	120	2	E45722	anti-glycoprotein
30	463.5	36.2	121	2	F37266	Ig heavy chain V r
31	462	36.1	139	2	PS0024	Ig heavy chain pre
32	461.5	36.1	113	2	PH0974	Ig heavy chain V r
33	461.5	36.1	119	2	PH0099	Ig heavy chain V r
34	460	36.0	113	2	S55534	Ig heavy chain V r
35	459.5	35.9	125	2	S20639	Ig heavy chain V r
36	459.5	35.9	138	2	PH0105	anti-digoxin trans
37	458.5	35.8	117	2	S03305	Ig heavy chain V r
38	458	35.8	120	2	S41394	Ig heavy chain V r
39	457	35.7	287	4	PC4402	pelB leader/Ig hea
40	456	35.7	150	2	PN0444	Ig heavy chain V r
41	456	35.7	246	2	S38950	Ig gamma chain - m
42	456	35.7	446	2	S40295	Ig gamma-2a chain
43	455	35.6	107	2	S09964	Ig kappa chain V-J
44	455	35.6	108	2	PH0975	Ig heavy chain V r
45	453.5	35.5	118	2	PL0200	anti-DNA autoantib

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identic
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match 57.2%; Score 731.5; DB 2; Length 268;
Best Local Similarity 58.8%; Pred. No. 4e-45;
Matches 143; Conservative 36; Mismatches 61; Indels 3; Gaps 3;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:||:|| :|||||||||:||  ||::    |||||||   : ||||||| | ||:| |
Db          3 QVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITKY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              : ||: || :  | || |||::| ||||||:|||||| |  :| |  :|||| |:|||||
Db         63 DPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCA-SYYLTRY-ENYWGQGTTVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||| :||||| | :||:|  :  | |::||::|:|| || | : |||||   ||
Db        121 GGGGSGGGDSGGGGSDIELTQSPAIMSASLGEKVTMSCRASSSV-NFIYWYQQKSDASPK 179

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              | : |||    ||| || ||| |  :: |||::: || | |:||| :|| ||| |||||
Db        180 LWVYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCQQFTSSPFTFGSGTKLE 239

Qy        241 IKR 243
              |||
Db        240 IKR 242
```

RESULT 2
S41374
single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antibody
A;Reference number: S41374

```
A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480

  Query Match           55.5%;  Score 710;  DB 2;  Length 249;
  Best Local Similarity  56.6%;  Pred. No. 1.3e-43;
  Matches  141;  Conservative   41;  Mismatches   59;  Indels    8;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||||  :||:||||||:|| |||::|    |:|||||    | |||| || | :|    |
Db          1 QVQLQQSGAELVRPGASVKLSCTASGFNFKDDYIHWVKQRPEKGLEWIARIAPASGNVKY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCA-RSTMITNYVMDYWGQVTSVTVS 119
                :|:||| :| | || |||: | ||||||:|||||| | |: |:  : |||| ::||||
Db         61 VPRFQDKATITADTSSNTAYLLLSSLTSEDTAVYYCARRDTLYTS--LGYWGQGSTVTVS 118

Qy        120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV-----SNDVAWYQQK 174
              | |||||||:||||| | :||:|  ::|  |: |:|:|::|:|:      : : |: |:
Db        119 SRGGGSGGGGSGGGGSDIELTQSPPSVVVIPGESVSISCRSSKSLLYSDGDSYLFWFLQR 178

Qy        175 PGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFG 234
              ||||| |||   |:  :|||||| ||| || ||  || ::|||: ||:| |    | |||
Db        179 PGQSPQLLIYRMSNLASGVPDRFSGSGSGTSFTLRISRVEAEDVGVYYCMQHREYPLTFG 238

Qy        235 GGTKLEIKR 243
                |||||:||
Db        239 AGTKLELKR 247


RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

  Query Match           50.5%;  Score 646;  DB 2;  Length 233;
  Best Local Similarity  55.2%;  Pred. No. 4.2e-39;
  Matches  133;  Conservative   27;  Mismatches   69;  Indels   12;  Gaps    3;

Qy          5 QQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKF 64
              |:|| :||: ||||||:||  ||::   |||||||:   : |||||||:| ||     :
Db          1 QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS 60

Qy         65 KDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGGGG 124
                || :| | || |||::| ||||||:|||||       |  |||||| |:|||||||||
Db         61 GVKATMTADTSSNTAYLQLSSLTSEDTAVYYC-------NAGMDYWGQGTTVTVSSGGGG 113

Qy        125 SGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND----VAWYQQKPGQSPT 180
              |||  :||||| | :||:|  | || | | ||:|:||:|||      : | |||||| |
Db        114 SGGRASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPPR 173

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              |||   |:  :||| || ||| |||||  |  :: || | |:||      ||||||
Db        174 LLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQH-IRELTRSEGGTKLE 232

Qy        241 I 241
              |
Db        233 I 233


RESULT 4
A49982
Ig heavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: A49982
R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Accession: A49982
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <LIN>
A;Cross-references: GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match           40.3%;  Score 516;  DB 2;  Length 120;
  Best Local Similarity  82.5%;  Pred. No. 3.6e-30;
  Matches   99;  Conservative    5;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||||||||||||||:||||||| ||||||| |:| || | |
Db          1 EVQLQQSGPELVKPGASVKISCKASGYSFTGYYIHWVKQSHVKSLEWIGHISPYNGATTY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              || ||| | ||||||||:||||| |||||||||||||     :| |||||| |||||||
Db         61 NQNFKDTASLTVDKSSTSAYMELHSLTSEDSAVYYCARFNYYGHYTMDYWGQGTSVTVSS 120


RESULT 5
I37267
Ig heavy chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: I37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: I37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match           39.2%;  Score 502;  DB 2;  Length 128;
  Best Local Similarity  79.7%;  Pred. No. 3.9e-29;
  Matches   98;  Conservative    7;  Mismatches   14;  Indels    4;  Gaps    1;

Qy          2 VQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYN 61
              ||||||||:|||||||||||| |||:|| | |||||||||||||| |||||| | ||
Db          6 VQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTSYN 65

Qy         62 QKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMIT----NYVMDYWGQVTSVT 117
              |||| || |||||||:||||||||||||||||||  : |    :|  ||||| |::|
Db         66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGLTTVVAKSYYFDYWGQGTTLT 125

Qy        118 VSS 120
              |||
Db        126 VSS 128


RESULT 6
PS0057
Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
```

```
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
A;Accession: PS0057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:g220449
A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             39.2%;  Score 501;  DB 2;  Length 135;
  Best Local Similarity   82.5%;  Pred. No. 4.8e-29;
  Matches   99;  Conservative    6;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||||||||||||||:|:||||||||||||||||||| || | |
Db         20 EVQLQQSGPELVKPGASVKISCKASGYSFTGYFMNWVKQSHGKSLEWIGRINPYNGDTFY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||:||||||||||||||||     ||    |||| | ||||:
Db         80 NQKFKGKATLTVDKSSSTAHMELRSLTSEDSAVYYCAR----LNYRGAYWGQGTLVTVSA 135


RESULT 7
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swit
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             38.9%;  Score 498;  DB 2;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 8.2e-29;
  Matches   96;  Conservative    8;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| | |||||||:|||||||| ||| |  | |
Db         20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSNGKSLEWIGYINPYNDYTSY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| ||||||||||||||  :  : | |||||| |||||||
Db         80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARYSYYSYYAMDYWGQGTSVTVSS 139


RESULT 8
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             38.8%;  Score 496.5;  DB 2;  Length 225;
  Best Local Similarity   87.5%;  Pred. No. 1.8e-28;
  Matches   98;  Conservative    3;  Mismatches   10;  Indels    1;  Gaps    1;

Qy        132 GGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYA 191
              |   |||||||| |||:||||||||||||||||||||||||||||||||| ||| | ||||
Db          9 GAHGSIVMTQTPKFLLLSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASSRYT 68

Qy        192 GVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLEIKR 243
              |||||| |||||||||||||:|||||||||||||:|  ||||||||||||
Db         69 GVPDRFTGSGYGTDFTFTISTVQAEDLAVYFCQQDYSS-YTFGGGTKLEIKR 119


RESULT 9
C37267
Ig heavy chain V region (Py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: C37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti-
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

  Query Match             38.6%;  Score 494;  DB 2;  Length 128;
  Best Local Similarity   77.2%;  Pred. No. 1.4e-28;
  Matches   95;  Conservative    9;  Mismatches   15;  Indels    4;  Gaps    1;

Qy          2 VQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYN 61
              ||||||||:|||||||:||||| |||:|| | |||||||||||||||| |||:| : ||
Db          6 VQLQQSGPELVKPGASMKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGRFNPNSGGSTYN 65

Qy         62 QKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCAR----STMITNYVMDYWGQVTSVT 117
              |||| || |||||||:|||||||||||||||||||||        |:|  |||||  |::|
Db         66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGPYGNYYTSYYFDYWGQGTTLT 125

Qy        118 VSS 120
              |||
Db        126 VSS 128


RESULT 10
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Residues: 1-151 <CHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchol
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
```

```
F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;137-151/Domain: C region (fragment) #status predicted <COR>

  Query Match             37.8%;  Score 483.5;  DB 2;  Length 151;
  Best Local Similarity   78.0%;  Pred. No. 9.6e-28;
  Matches   96;  Conservative    7;  Mismatches   11;  Indels    9;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|:||||||||||||||:|| | ||||||||||||||  :||   | |
Db         20 EVQLQQSGPELLKPGASVKISCKASGYTFTDYTMHWVKQSHGKSLEWIGGFDPNYDNTFY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY---VMDYWGQVTSVT 117
              |:|||||| |||||||||||||||||||||||||      :|    :|||| ||||
Db         80 NEKFKDKATLTVDKSSTTAYMELRSLTSEDSAVYYCA------SYDYGALDYWGQGTSVT 133

Qy        118 VSS 120
              |||
Db        134 VSS 136


RESULT 11
B30502
Ig heavy chain V region (D444) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: B30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: B30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-144 <EIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             37.6%;  Score 481.5;  DB 2;  Length 144;
  Best Local Similarity   59.1%;  Pred. No. 1.3e-27;
  Matches   97;  Conservative   16;  Mismatches   28;  Indels   23;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||: ||| ||||||  |: | ||| ||| |  | |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTITGYVMHWVKQRPGQGLAWIGYINPYNDGTKY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |:||| || || |||||:||| || || ||||| |||||         |||||  |::||
Db         61 NEKFKGKATLTSDKSSSTAYTELSSLASEDSAAYYCARGG------FDYWGQGTTLTV-- 112

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV 164
                          |::||:|  | || |:||: :|:||||:
Db        113 --------------DILLTQSPAILSVSPGERVSFSCRASQSI 141


RESULT 12
S26319
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26319
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26319
A;Molecule type: mRNA
A;Residues: 1-114 <STA>
A;Cross-references: EMBL:X59172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>

  Query Match             37.6%;  Score 481;  DB 2;  Length 114;
  Best Local Similarity   80.5%;  Pred. No. 1.1e-27;
  Matches   95;  Conservative    6;  Mismatches   11;  Indels    6;  Gaps    2;

Qy          5 QQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKF 64
              |||||:|||||||||||||||||||:|:|||||||||||||||| || | |||||
Db          1 QQSGPELVKPGASVKISCKASGYSFTGYFMNWVKQSHGKSLEWIGRINPYNGDTFYNQKF 60

Qy         65 KDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY--VMDYWGQVTSVTVSS 120
              | || |||||||:||:||| |||||||||||| :      |   |||||| |||||||
Db         61 KGKATLTVDKSSSTAHMELLSLTSEDSAVYYCGKD----GYYGAMDYWGQGTSVTVSS 114


RESULT 13
MHMS4E
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02039
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain cor
A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Accession: A02039
A;Molecule type: protein
A;Residues: 1-117 <KEH>
A;Cross-references: UNIPROT:P01756
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context ar
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical

  Query Match             37.6%;  Score 480.5;  DB 1;  Length 117;
  Best Local Similarity   78.3%;  Pred. No. 1.2e-27;
  Matches   94;  Conservative    8;  Mismatches   15;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| ||| |||||||||||||| |||||| | |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| ||||||||||||||     ::  | ||  |:|||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD---YDWYFDVWGAGTTVTVSS 117


RESULT 14
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T01407
R;Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamotc
Microbiol. Immunol. 36, 855-863, 1992
A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A;Reference number: Z14317; MUID:93116638; PMID:1474935
A;Accession: T01407
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-140 <TAK>
A;Cross-references: EMBL:S51851; NID:g262657
C;Superfamily: immunoglobulin V region; immunoglobulin homology

  Query Match             37.6%;  Score 480.5;  DB 2;  Length 140;
  Best Local Similarity   78.3%;  Pred. No. 1.5e-27;
  Matches   94;  Conservative    8;  Mismatches   15;  Indels    3;  Gaps    1;
```

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:||.||| ||||||||||||| |||||| | |
Db         20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| |||||||||||||     ::  | ||  |:|||||
Db         80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD---YDWYFDVWGAGTTVTVSS 136


RESULT 15
MHMSJ5
Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26242
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A;Reference number: A26242; MUID:80078170; PMID:6765983
A;Accession: A26242
A;Molecule type: protein
A;Residues: 1-117 <SCH>
A;Cross-references: UNIPROT:P01757
A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             37.5%;  Score 479.5;  DB 1;  Length 117;
  Best Local Similarity   78.3%;  Pred. No. 1.4e-27;
  Matches   94;  Conservative    7;  Mismatches   16;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| ||| |||||||||||||| |||||| | |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| |||||||||||||      :  | ||  |:|||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY---WYFDVWGAGTTVTVSS 117


Search completed: March 11, 2005, 14:56:09
Job time : 23 secs
```

OM protein - protein search, using sw model

Run on: March 11, 2005, 14:48:42 ; Search time 63 Seconds
(without alignments)
1975.163 Million cell updates/sec

Title: US-10-016-686-1
Perfect score: 1279
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....QQDYNSPPTFGGGTKLEIKR 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	828.5	64.8	243	2	Q7TQM2	Q7tqm2 mus musculu
2	780.5	61.0	244	2	Q65ZC8	Q65zc8 homo sapien
3	753.5	58.9	255	2	Q6KB05	Q6kb05 mus musculu
4	743.5	58.1	487	2	Q65ZL2	Q65zl2 mus sp. fv/
5	702	54.9	298	2	Q9QYF0	Q9qyf0 synthetic c
6	701.5	54.8	241	2	Q921A6	Q921a6 mus musculu
7	698.5	54.6	240	2	Q65ZC9	Q65zc9 homo sapien
8	655	51.2	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
9	577	45.1	218	2	Q925S1	Q925s1 mus musculu
10	507.5	39.7	117	2	Q9QXE9	Q9qxe9 mus musculu
11	501.5	39.2	170	2	Q925S2	Q925s2 mus musculu
12	499	39.0	470	2	Q7TMK1	Q7tmk1 mus musculu
13	497.5	38.9	117	2	Q9QXF0	Q9qxf0 mus musculu
14	491.5	38.4	134	2	Q65ZR6	Q65zr6 mus musculu
15	491	38.4	472	2	Q6PJA7	Q6pja7 mus musculu
16	484	37.8	145	2	Q924Q9	Q924q9 mus musculu
17	483	37.8	145	2	Q924Q6	Q924q6 mus musculu
18	480.5	37.6	117	1	HV12_MOUSE	P01756 mus musculu
19	479.5	37.5	117	1	HV13_MOUSE	P01757 mus musculu
20	479	37.5	118	1	HV51_MOUSE	P06330 mus musculu
21	476	37.2	145	2	Q924R4	Q924r4 mus musculu
22	468	36.6	99	2	Q9JL74	Q9jl74 mus musculu
23	468	36.6	145	2	Q924R1	Q924r1 mus musculu
24	467.5	36.6	146	2	Q924Q3	Q924q3 mus musculu
25	465.5	36.4	488	2	Q91WR1	Q91wr1 mus musculu
26	464.5	36.3	123	2	Q8VIJ1	Q8vij1 mus musculu
27	464	36.3	145	2	Q924P7	Q924p7 mus musculu
28	463	36.2	143	2	Q924R0	Q924r0 mus musculu
29	456.5	35.7	142	2	Q924Q1	Q924q1 mus musculu
30	456	35.7	143	2	Q924P6	Q924p6 mus musculu
31	455.5	35.6	140	2	Q924R2	Q924r2 mus musculu
32	454.5	35.5	146	2	Q924R8	Q924r8 mus musculu
33	453.5	35.5	488	2	Q8K0F2	Q8k0f2 mus musculu
34	452.5	35.4	482	2	Q8K172	Q8k172 mus musculu
35	451	35.3	139	1	HV07_MOUSE	P01751 mus musculu
36	451	35.3	145	2	Q924Q7	Q924q7 mus musculu
37	449	35.1	145	2	Q924R3	Q924r3 mus musculu
38	447.5	35.0	146	2	Q924Q8	Q924q8 mus musculu
39	445	34.8	137	2	Q924R6	Q924r6 mus musculu
40	441.5	34.5	120	2	Q920E8	Q920e8 mus musculu
41	441	34.5	141	2	Q924Q4	Q924q4 mus musculu
42	440.5	34.4	140	2	Q924P8	Q924p8 mus musculu
43	437	34.2	143	2	Q924R7	Q924r7 mus musculu
44	434.5	34.0	473	2	Q9D8L4	Q9d8l4 mus musculu
45	432.5	33.8	465	2	Q6PJB2	Q6pjb2 mus musculu

ALIGNMENTS

RESULT 1
Q7TQM2
ID Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ScFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 1
SQ SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;

Query Match. 64.8%; Score 828.5; DB 2; Length 243;
Best Local Similarity 66.1%; Pred. No. 4.1e-58;
Matches 160; Conservative 30; Mismatches 47; Indels 5; Gaps 2;

```
Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||| :||:||||||:|||||||:|| |:|||||| ||: ||||| | | :|:| |
Db          1 QVQLQQSGSELVRPGASVKLSCKASGYTFTTYWMHWVKQRHGQGLEWIGNIYPGSGITNY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ::|||:| ||||| ||:|||| | || |||||||||||       :| ||  |::||||
Db         61 DEKFKNKGILTVDTSSSTAYMHLSSLASEDSAVYYCARG----GRGLDVWGAGTTLTVSS 116

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | |||: :   || |||||||||||: : | :|||||||| :|
Db        117 GGGGSGGGGSGGGGSDIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPR 176

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||||  :|   ||| || ||| | |:| :|::|| ||:| |:||| | |  |||||||||
Db        177 LLISGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQ-YWSTRTFGGGTKLE 235

Qy        241 IK 242
              ||
Db        236 IK 237
```

```
RESULT 2
Q65ZC8
ID   Q65ZC8      PRELIMINARY;      PRT;   244 AA.
AC   Q65ZC8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13057; CAA73500.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     244    244
SQ   SEQUENCE   244 AA;  26127 MW;  4B1F17868338F2BF CRC64;

  Query Match             61.0%;  Score 780.5;  DB 2;  Length 244;
  Best Local Similarity   61.5%;  Pred. No. 2.7e-54;
  Matches  150;  Conservative   35;  Mismatches   58;  Indels    1;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||| ||| :: ||| |||:|||||||:|: :|||||:|: |: |||:| |:|||| | :
Db          1 QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEWMGWIDPNNGDTRF 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCAR-STMITNYVMDYWGQVTSVTVS 119
               |:|: :  :| | | : ||||:  | |:|:|||||||  |    | || ||| | ||||
Db         61 AQRFQGRVTMTRDTSISAAYMEVSRLRSDDTAVYYCAREGTGSAIYGMDVWGQGTLVTVS 120

Qy        120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSP 179
              |||||||||:||||| | |||:|: |  | ||||||||:||: : : :||||||||::|
Db        121 SGGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAP 180

Qy        180 TLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKL 239
                ||   ||  :| | || ||| ||||| |||:|| :| | |:|||  | | ||||||||
Db        181 KFLIYKASSLASGAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKL 240

Qy        240 EIKR 243
              ||||
Db        241 EIKR 244


RESULT 3
Q6KB05
ID   Q6KB05      PRELIMINARY;      PRT;   255 AA.
AC   Q6KB05;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ScFv B8E5 protein (Fragment).
GN   Name=scFv B8E5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RA   Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA   Briand J.P., Hoebeke J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ746180; CAG34081.1; -.
DR   HSSP; P01837; 1KCR.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
SQ   SEQUENCE   255 AA;  27445 MW;  B68BD38395DF713B CRC64;

  Query Match             58.9%;  Score 753.5;  DB 2;  Length 255;
  Best Local Similarity   57.9%;  Pred. No. 4.1e-52;
  Matches  146;  Conservative   37;  Mismatches   56;  Indels   13;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||||| |||||| |:|:|| |||::|: | | ||:|:  | |||:  |      | |
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY----VMDYWGQVTSV 116
                  | :  :: | :  | |::: || |||:|:|||||     ||      ||||| |::
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARH---INYRYDGAFDYWGQGTTL 117

Qy        117 TVSSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND------VAW 170
              ||||||||||||:||||| ||| |:|: | ||||::| ::||:|||: |       :||
Db        118 TVSSGGGGSGGGGSGGGGSDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAW 177

Qy        171 YQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSP 230
              |||||||||  |||    |:| :|||||| ||| ||||| |||::|||||||:|| |:: |
Db        178 YQQKPGQSPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYP 237

Qy        231 PTFGGGTKLEIK 242
              ||| |||||||
Db        238 LTFGAGTKLEIK 249


RESULT 4
Q65ZL2
ID   Q65ZL2      PRELIMINARY;      PRT;   487 AA.
AC   Q65ZL2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   FV/M4.
GN   Name=M4-IFN-<tau>;
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96272580; PubMed=8688499;
RA   Qi Y., Xiang J.;
RT   "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT   antibody secreted from myeloma cells.";
RL   Hum. Antibodies Hybridomas 6:161-166(1995).
DR   EMBL; S82493; AAB37424.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 4.
```

```
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   487 AA;  53578 MW;  C7BAB69F30555504 CRC64;

  Query Match             58.1%;  Score 743.5;  DB 2;  Length 487;
  Best Local Similarity   59.5%;  Pred. No. 5.4e-51;
  Matches  144;  Conservative   37;  Mismatches   54;  Indels    7;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :||||||  :|||||||||||||||||:|| : :|| ||   : ||||| |:| |    |
Db         20 QVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              |:||| || || ||||:||||:| ||||||||||:| ||          :||| |::|  |
Db         80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRS------YYGHWGQGTTLT-GS 132

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | |||:|  | || |: |||||:||::: :::|||||| |:||
Db        133 GGGGSGGGGSGGGGSRIQMTQSPASLSVSVGELVTITCRASENIYSNLAWYQQKQGKSPQ 192

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||:   ::   ||| || ||| || ::  |::||:||   |:||  : :| ||||||:||
Db        193 LLVYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTRLE 252

Qy        241 IK 242
              ||
Db        253 IK 254


RESULT 5
Q9QYF0
ID   Q9QYF0      PRELIMINARY;      PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CN 8 single chain antibody.
GN   Name=CN 8 scFv;
OS   synthetic construct.
OC   other sequences; artificial sequences.
OX   NCBI_TaxID=32630;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;
RA   Shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a vascular cell wall-specific monoclonal antibody
RT   recognizing a cell polarity by using a phage display subtraction
RT   method.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR   EMBL; AB036341; BAA88633.1; -.
DR   PIR; A33933; A33933.
DR   PIR; S19112; S19112.
DR   HSSP; P01820; 1A7O.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;

  Query Match             54.9%;  Score 702;  DB 2;  Length 298;
  Best Local Similarity   54.3%;  Pred. No. 6.2e-48;
  Matches  132;  Conservative   41;  Mismatches   68;  Indels    2;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:|||||  |||||  |:|:|| |||  |: |:| ||:|: || |||||  |||::    |
Db         40 QVKLQQSGGGLVKPGGSLKLSCAASGSDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 99

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                  ||| |:: | :  | |:::  : |||:|:|||||::   :    |||| |:|||||
Db        100 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYYGHSA--YWGQGTTVTVSS 157

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:|  |  | |: |||||:|| :: | :|||||| |:||
Db        158 GGGGSGGGGSGGGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQ 217

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              ||:   :  |||| || ||| || ::  |::||  ||   |:||  : :| ||||||||||
Db        218 LLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLE 277

Qy        241 IKR 243
              |||
Db        278 IKR 280


RESULT 6
Q921A6
ID   Q921A6      PRELIMINARY;      PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-CEA 79 single chain Fv (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
DR   EMBL; U88067; AAB48044.1; -.
DR   PIR; S19965; S19965.
DR   PIR; S19967; S19967.
DR   PIR; S19968; S19968.
DR   PIR; S26325; S26325.
DR   HSSP; P01607; 1BWW.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     241    241
SQ   SEQUENCE   241 AA;  26086 MW;  0276887248E9C771 CRC64;

  Query Match             54.8%;  Score 701.5;  DB 2;  Length 241;
  Best Local Similarity   54.3%;  Pred. No. 5.3e-48;
  Matches  133;  Conservative   47;  Mismatches   58;  Indels    7;  Gaps    4;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:||||||:| ||| :||||||||||:|| | |:|||: || |:|:| ||   |   |
Db          1 QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                 || :   ::: |::|||::: :| :||:| |:|||  ::  :  ||||| |:|||||
Db         61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARKDLLRYF--DYWGQGTTVTVSS 118

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | :||:|: |   | | :||||||||| ::  :|||| |||: |
Db        119 GGGGSGGGGSGGGGSDIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPR 178

Qy        181 LLISYTSSRY--AGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
                ::|   |   |:| || ||| | |::|:|| |: ||:| |:|   |::  |||||||
Db        179 --SAHTLHIYIQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLH-YDNLHTFGGGTK 235

Qy        239 LEIKR 243
              ||:||
Db        236 LELKR 240


RESULT 7
Q65ZC9
ID   Q65ZC9      PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
```

```
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             54.6%;  Score 698.5;  DB 2;  Length 240;
  Best Local Similarity   56.0%;  Pred. No. 9.2e-48;
  Matches  136;  Conservative   36;  Mismatches   68;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|||:|||  ||:|| |:::|| |||::|: | ||||:|: || |||:  |: :     |
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                 | :  :: | |  | |::: || :||:|||||||        :| ||: | |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD---WGDSLDPWGKGTLVTVSS 117

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
              |||||||||:||||| | |||:|: |  | ||||||||:||: :   :||||||||::|
Db        118 GGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQQKPGKAPK 177

Qy        181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
              |||   ||  :  | || ||| ||||| |||:|| :| | |:|||  | | |||||||||
Db        178 LLIYKASSLASRAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 237

Qy        241 IKR 243
              |||
Db        238 IKR 240


RESULT 8
Q65ZQ7
ID   Q65ZQ7      PRELIMINARY;      PRT;   248 AA.
AC   Q65ZQ7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   B3(Fv)-PE40 (Fragment).
GN   Name=B3(Fv)-PE40;
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92020904; PubMed=1924323;
RA   Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT   "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT   regression of a human carcinoma in mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR   EMBL; S57990; AAB19971.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER     248    248
SQ   SEQUENCE   248 AA;  26634 MW;  7A3759B43E570950 CRC64;

  Query Match             51.2%;  Score 655;  DB 2;  Length 248;
  Best Local Similarity   51.8%;  Pred. No. 2.8e-44;
  Matches  128;  Conservative   45;  Mismatches   68;  Indels    6;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:| :||  ||:|| |:|:||  ||::|: |||:||:|:  | |||:  |: ::    |
Db          2 DVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTPEKRLEWVAYISNDDSSAAY 61

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                 | :  :: | :  | |::  | |||:|:| |||  :       |||| | |||||
Db         62 SDTVKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARG-LAWGAWFAYWGQGTLVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQKP 175
              |||||||||:||||| ::|||:|  | || ||: :|:|::|| :  ||    : || |||
Db        121 GGGGSGGGGSGGGGSDVLMTQSPLSLPVSLGDQASISCRSSQIIVHSNGNTYLEWYLQKP 180

Qy        176 GQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGG 235
              |||| |||   |:|::|||||| ||| |||||  || ::|||| ||:| |  : | |||
Db        181 GQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGS 240

Qy        236 GTKLEIK 242
              |||||||
Db        241 GTKLEIK 247


RESULT 9
Q925S1
ID   Q925S1      PRELIMINARY;      PRT;   218 AA.
AC   Q925S1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MRP5 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA   Su C.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR   EMBL; AF240168; AAK43733.1; -.
DR   HSSP; P01665; 1QNZ.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     218    218
SQ   SEQUENCE   218 AA;  23013 MW;  527E4FA8F7982817 CRC64;

  Query Match             45.1%;  Score 577;  DB 2;  Length 218;
  Best Local Similarity   51.4%;  Pred. No. 4e-38;
```

```
  Matches  112;  Conservative   42;  Mismatches   58;  Indels    6;  Gaps    2;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:||||||:| ||| :|:||||||||:||    | ||::  || |:||| || ::||  |
Db          3 QVKLQQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINTHSGVPKY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ::|| :   ::: |::|||::: :| :||:| |:| |     :   |||| |:|||||
Db         63 AEEFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMRWDYDGGFA--YWGQGTTVTVSS 120

Qy        121 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSN----DVAWYQQKPG 176
              |||||||||:| ||| ||:||:|  | || | | ||:|:||:|| |     : |:|||||
Db        121 GGGGSGGGGSGSGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMNWFQQKPG 180

Qy        177 QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQ 214
              | | |||   | : :|||   : || ||||:  |  ::
Db        181 QPPKLLIYAASKQGSGVPAGLLASGSGTDFSLNIYPME 218


RESULT 10
Q9QXE9
ID   Q9QXE9      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   PIR; F33932; F33932.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     117     117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;

  Query Match             39.7%;  Score 507.5;  DB 2;  Length 117;
  Best Local Similarity   82.5%;  Pred. No. 6.8e-33;
  Matches   99;  Conservative    5;  Mismatches   13;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| ||| |||||||||||||| |||||| | |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| ||||||||||||||      | |||||| |||||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY---YAMDYWGQGTSVTVSS 117


RESULT 11
Q925S2
ID   Q925S2      PRELIMINARY;      PRT;   170 AA.
AC   Q925S2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MRP4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA   Su C.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR   EMBL; AF240167; AAK43732.1; -.
DR   HSSP; P01751; 1A6W.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   170 AA;  17978 MW;  5042823CC6C10F38 CRC64;

  Query Match             39.2%;  Score 501.5;  DB 2;  Length 170;
  Best Local Similarity   69.1%;  Pred. No. 3.1e-32;
  Matches   94;  Conservative   17;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              :|:||||||::|:|| ||||||| |||:|| | |||:| :| :|||||| |:  :| | |
Db          3 QVKLQQSGPEVVRPGVSVKISCKGSGYTFTDYSMHWLKMNHAQSLEWIGIISTYDGNTNY 62

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN-YVMDYWGQVTSVTVS 119
              ||||| || :|||||| ||||||  |||:|||:|||||     : |  ||||| |:||||
Db         63 NQKFKGKATMTVDKSSITAYMELARLTSDDSAIYYCARGAYYGSFYYFDYWGQGTTVTVS 122

Qy        120 SGGGGSGGGGTGGGGS 135
              ||||||||||:|||||
Db        123 SGGGGSGGGGSGGGGS 138


RESULT 12
Q7TMK1
ID   Q7TMK1      PRELIMINARY;      PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

```
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -.
DR   HSSP; P01865; 1KB5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51727 MW;  6D90E4DF896BB090 CRC64;

  Query Match             39.0%;  Score 499;  DB 2;  Length 470;
  Best Local Similarity   63.4%;  Pred. No. 1.6e-31;
  Matches  104;  Conservative   11;  Mismatches   27;  Indels   22;  Gaps    3;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||||||||||:||||||||||||||||||| :||:|| | |
Db         20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY-VMDYWGQVTSVTVS 119
              ||||| || |||||||:|||||| ||||||||||||||     :|    | ||  |:||||
Db         80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139

Qy        120 SGGGGSGGGGTGGGGSSIVMTQTPTFLLV-----SAGDRVTITC 158
              |                |  : ||     ::|  ||: |
Db        140 SA----------------TTTAPSVYPLVPGCGDTSGSSVTLGC 167


RESULT 13
Q9QXF0
ID   Q9QXF0      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   PIR; PH0973; PH0973.
DR   HSSP; P01751; 1NQB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     117     117
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD0858A47E4C CRC64;

  Query Match             38.9%;  Score 497.5;  DB 2;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 4.3e-32;
  Matches   96;  Conservative    8;  Mismatches   13;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| ||| |||||||||||||| |||||| | |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:|||||||:|| ||| |||||||||||||| |||||| |::||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD---KDYYFDYWGQGTTLTVSS 117


RESULT 14
Q65ZR6
ID   Q65ZR6      PRELIMINARY;      PRT;   134 AA.
AC   Q65ZR6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Ab 126.33 heavy chain variable and joining regions (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91237115; PubMed=1709665;
RA   Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT   "Junctional diversity of H and L chains allows the coexpression of two
RT   mutually exclusive idiotopes (IdI104 and IdI558).";
RL   J. Immunol. 146:4024-4030(1991).
DR   EMBL; M74139; AAA37776.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   134 AA;  14908 MW;  1852D86D26FC7567 CRC64;

  Query Match             38.4%;  Score 491.5;  DB 2;  Length 134;
  Best Local Similarity   80.0%;  Pred. No. 1.5e-31;
  Matches   96;  Conservative    8;  Mismatches   13;  Indels    3;  Gaps    1;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:|||||||||:|||||||:|| ||| |||||| |||||||| |||||| | |
Db         18 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSPGKSLEWIGDINPNNGGTSY 77

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
              ||||| || |||||||:||||:| ||||||||||||||     :|| ||||| |::||||
Db         78 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD---YSYVFDYWGQGTTLTVSS 134


RESULT 15
Q6PJA7
ID   Q6PJA7      PRELIMINARY;      PRT;   472 AA.
AC   Q6PJA7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
```

```
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -.
DR   HSSP; P01865; 1KB5.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  52299 MW;  165169C23D55D4AB CRC64;

  Query Match             38.4%;  Score 491;  DB 2;  Length 472;
  Best Local Similarity   51.1%;  Pred. No. 7e-31;
  Matches  112;  Conservative   20;  Mismatches   49;  Indels   38;  Gaps    5;

Qy          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY 60
              |||||||||:||| |||||:|||||||:|: ||||||||||||||||| | ||||    |
Db         20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy         61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCAR---STMITNYVMDYWGQVTSVT 117
              ||||| || |||||||:||||||||||||||||||||   |    ::  ||||| |::|
Db         80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYYSYDHYFDYWGQGTTIT 139

Qy        118 VSSG--------------GGGSGGGGTGG--------------GGSSIVMTQTPTFLLVS 149
              |||                |  :|   | |               |  : :   ||  |
Db        140 VSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVL 199

Qy        150 AGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSS 188
                |  |::   : : |    |    | || |  ::: :|
Db        200 QSDLYTLSSSVTVTSS---TW----PSQSITCNVAHPAS 231


Search completed: March 11, 2005, 14:55:45
Job time : 68 secs
```

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 14:58:51 ; Search time 3609 Seconds
(without alignments)
9787.712 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	728.2	99.9	729	6	BD136150	BD136150 Vector. 9
2	728.2	99.9	729	6	AX002778	AX002778 Sequence
3	728.2	99.9	729	6	AX149544	AX149544 Sequence
4	727.4	99.8	729	6	BD136268	BD136268 Enhanceme
5	727.4	99.8	729	6	AX018532	AX018532 Sequence
6	727.4	99.8	729	6	AX018608	AX018608 Sequence
7	727.4	99.8	1807	6	BD136151	BD136151 Vector. 9
8	727.4	99.8	1807	6	AX002779	AX002779 Sequence
9	724.4	99.4	1467	6	BD136152	BD136152 Vector. 9
10	724.4	99.4	1467	6	AX002780	AX002780 Sequence
11	724.4	99.4	1467	6	AX149546	AX149546 Sequence
12	724.2	99.3	1518	6	BD136154	BD136154 Vector. 9
13	724.2	99.3	1518	6	AX002782	AX002782 Sequence
14	724.2	99.3	1518	6	AX149550	AX149550 Sequence
15	721	98.9	1796	6	AX149547	AX149547 Sequence
16	721	98.9	2090	6	BD136155	BD136155 Vector. 9
17	721	98.9	2090	6	AX002783	AX002783 Sequence
18	721	98.9	2090	6	AX149551	AX149551 Sequence
19	481.2	66.0	10511	6	AX666316	AX666316 Sequence
20	463.6	63.6	804	6	CQ868387	CQ868387 Sequence
21	462	63.4	723	12	AF332008	AF332008 Synthetic
22	458.2	62.9	756	6	A76868	A76868 Sequence 6
23	458.2	62.9	756	6	AR456298	AR456298 Sequence
24	456	62.6	729	10	AF002242	AF002242 Mus muscu
25	450.8	61.8	735	12	AF162710	AF162710 Synthetic
26	442	60.6	1725	6	AX001509	AX001509 Sequence
27	441.2	60.5	735	12	SCO250760	AJ250760 Mus muscu
28	440.6	60.4	753	12	SCO416563	AJ416563 Synthetic
29	439.4	60.3	1701	12	SCO564232	AJ564232 Synthetic
30	438.8	60.2	864	6	A83227	A83227 Sequence 47
31	438.8	60.2	864	6	AR182952	AR182952 Sequence
32	438.8	60.2	864	6	BD096925	BD096925 Chemical
33	438.8	60.2	2019	6	A83211	A83211 Sequence 31
34	438.8	60.2	2019	6	AR182939	AR182939 Sequence
35	438.8	60.2	2019	6	BD096912	BD096912 Chemical
36	438.8	60.2	2025	6	A83217	A83217 Sequence 37
37	438.8	60.2	2025	6	AR182944	AR182944 Sequence
38	438.8	60.2	2025	6	BD096917	BD096917 Chemical
39	438.6	60.2	1668	6	AX001511	AX001511 Sequence
40	438.6	60.2	2438	6	CQ812173	CQ812173 Sequence
41	438.2	60.1	828	6	BD174830	BD174830 Antibody-
42	437.8	60.1	726	6	AX100174	AX100174 Sequence
43	432.8	59.4	795	12	AF329093	AF329093 Synthetic
44	432.8	59.4	810	6	CQ832138	CQ832138 Sequence
45	432.8	59.4	810	6	CQ832288	CQ832288 Sequence

ALIGNMENTS

RESULT 1
BD136150
LOCUS BD136150 729 bp DNA linear PAT 18-SEP-2002
DEFINITION Vector.
ACCESSION BD136150
VERSION BD136150.1 GI:23231095
KEYWORDS JP 2002507117-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 729)
AUTHORS Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and Myers,K.A.
TITLE Vector
JOURNAL Patent: JP 2002507117-A 1 05-MAR-2002;
OXFORD BIOMEDICA LTD
COMMENT OS Artificial Sequence
PN JP 2002507117-A/1
PD 05-MAR-2002
PF 04-JUN-1998 JP 1999501858
PR 04-JUN-1997 GB 9711579.4,20-JUN-1997 GB 9713150.2 PR 04-JUL-1997 GB 9714230.1
PI SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA PI MARGARET ELLARD,
PI MILES WILLIAM CARROLL,KEVIN ALAN MYERS
PC C12N15/85,A61K48/00
CC Description of Artificial Sequence: DNA
FH Key Location/Qualifiers
FT source 1. .729
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 99.9%; Score 728.2; DB 6; Length 729;
Best Local Similarity 100.0%; Pred. No. 2.7e-219;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

```
                                                                                
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                                                                                
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                                                                                
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                                                                                
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                                                                                
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                                                                                
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                                                                                
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                                                                                
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                                                                                
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                                                                                
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                                                                                
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                                                                                
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
                                                                                
Db        721 ATCAAACGG 729


RESULT 2
AX002778
LOCUS       AX002778                729 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9855607.
ACCESSION   AX002778
VERSION     AX002778.1  GI:9885103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 1 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             <1. .>729
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04191.1"
                     /db_xref="GI:9885104"
                     /translation="EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKS
                     LEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI
                     TNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKA
                     SQSVSNDVXWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDL
                     AVYFCQQDYNSPPTFGGGTKLEIKR"
ORIGIN

  Query Match           99.9%;  Score 728.2;  DB 6;  Length 729;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-219;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
                                                                                
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                                                                                
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                                                                                
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                                                                                
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                                                                                
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                                                                                
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                                                                                
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                                                                                
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                                                                                
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                                                                                
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                                                                                
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                                                                                
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
                                                                                
Db        721 ATCAAACGG 729


RESULT 3
```

```
AX149544
LOCUS       AX149544                729 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 5 from Patent WO0136486.
ACCESSION   AX149544
VERSION     AX149544.1  GI:14347983
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 5 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5T4ScFv.1"
ORIGIN

  Query Match             99.9%;  Score 728.2;  DB 6;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-219;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 4
BD136268
LOCUS       BD136268                729 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Enhancement of prodrug activation.
ACCESSION   BD136268
VERSION     BD136268.1  GI:23231213
KEYWORDS    JP 2002505341-A/21.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 729)
  AUTHORS   Stratford,I.J., Patterson,A.V., Kingsman,S.M., Kan,O., Griffiths,L.
            and Mitrophanous,K.
  TITLE     Enhancement of prodrug activation
  JOURNAL   Patent: JP 2002505341-A 21 19-FEB-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002505341-A/21
            PD   19-FEB-2002
            PF   05-MAR-1999 JP 2000534657
            PR   06-MAR-1998 GB    9804841.6,19-AUG-1998 GB    9818103.5 PR
            29-JAN-1999 GB    9902081.0
            PI   IAN JAMES STRATFORD,ADAM VORN PATTERSON,SUSAN MARY KINGSMAN,ON

            PI   KAN,
            PI   LEIGH GRIFFITHS,KYRIACOS MITROPHANOUS
            PC   A61K47/48,A61K35/76,A61K38/44,A61K45/00,A61K48/00,A61P9/10, PC
              A61P29/00,
            PC   A61P35/00,A61P43/00,C12N5/10,C12N7/00,C12N9/02,C12N15/09, PC
            A61K37/50,
            PC   C12N5/00,C12N15/00
            CC   Description of Artificial Sequence: Synthetic sequence FH
            Key             Location/Qualifiers
            FT   source          1. .729
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             99.8%;  Score 727.4;  DB 6;  Length 729;
  Best Local Similarity   99.9%;  Pred. No. 4.8e-219;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
```

```
Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 5
AX018532
LOCUS AX018532 729 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent WO9945127.
ACCESSION AX018532
VERSION AX018532.1 GI:10042675
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J., Griffiths,L. and Kan,O.
TITLE Enhanced prodrug activation
JOURNAL Patent: WO 9945127-A 26 10-SEP-1999;
KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN ON (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 99.8%; Score 727.4; DB 6; Length 729;
Best Local Similarity 99.9%; Pred. No. 4.8e-219;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 6
AX018608
LOCUS AX018608 729 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 26 from Patent WO9945126.
ACCESSION AX018608
VERSION AX018608.1 GI:10042738
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J., Griffiths,L. and Kan,O.
TITLE Enhanced prodrug activation
JOURNAL Patent: WO 9945126-A 26 10-SEP-1999;
KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN ON (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES Location/Qualifiers
source 1. .729
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 99.8%; Score 727.4; DB 6; Length 729;
Best Local Similarity 99.9%; Pred. No. 4.8e-219;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

```
RESULT 7
BD136151
LOCUS       BD136151                1807 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136151
VERSION     BD136151.1  GI:23231096
KEYWORDS    JP 2002507117-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1807)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 2 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/2
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: cDNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1807
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1807
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN
```

```
  Query Match             99.8%;  Score 727.4;  DB 6;  Length 1807;
  Best Local Similarity   99.9%;  Pred. No. 5.2e-219;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

```
RESULT 8
```

```
AX002779
LOCUS       AX002779               1807 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9855607.
ACCESSION   AX002779
VERSION     AX002779.1  GI:9885105
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 2 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1807
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             <3. .1790
                     /note="unnamed protein product; cDNA"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04205.1"
                     /db_xref="GI:9885106"
                     /translation="ASTMGWSCIILFLVATATGVHSEVQLQQSGPDLVKPGASVKISC
                     KASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAY
                     MELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIV
                     MTQTPTFLLVSAGDRVTIITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDR
                     FIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLEIKRASTKGPSVFPL
                     APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
                     TVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
                     PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
                     VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                     NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                     QGNVFSCSVMHEALHNHYTQKSLSLSPGK"
ORIGIN

  Query Match           99.8%;  Score 727.4;  DB 6;  Length 1807;
  Best Local Similarity  99.9%;  Pred. No. 5.2e-219;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 9
BD136152
LOCUS       BD136152               1467 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136152
VERSION     BD136152.1  GI:23231097
KEYWORDS    JP 2002507117-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1467)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 3 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/3
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1467
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           99.4%;  Score 724.4;  DB 6;  Length 1467;
  Best Local Similarity  99.9%;  Pred. No. 4.6e-218;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858
```

```
Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

```
RESULT 10
AX002780
LOCUS       AX002780                1467 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 3 from Patent WO9855607.
ACCESSION   AX002780
VERSION     AX002780.1  GI:9885107
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 3 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             1. .1467
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC04192.1"
                     /db_xref="GI:9885108"
                     /translation="MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKE
                     VATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIV
                     ILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNIRRI
                     ICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLI
                     KYGHLRVNQTFNWNTTKQEHFPDGGGGSEVQLQQSGPDLVKPGASVKISCKASGYSFT
                     GYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAYMELRSLTS
                     EDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGGGGSGGGGTGGGGSSIVMTQTPTFL
                     LVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGT
                     DFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLEIK"
ORIGIN
```

```
  Query Match           99.4%;  Score 724.4;  DB 6;  Length 1467;
  Best Local Similarity 99.9%;  Pred. No. 4.6e-218;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

```
RESULT 11
AX149546
LOCUS       AX149546                1467 bp    DNA     linear   PAT 08-JUN-2001
```

```
DEFINITION  Sequence 7 from Patent WO0136486.
ACCESSION   AX149546
VERSION     AX149546.1  GI:14347985
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 7 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1467
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="B7-1.5T4ScFv.1"
ORIGIN

  Query Match            99.4%;  Score 724.4;  DB 6;  Length 1467;
  Best Local Similarity  99.9%;  Pred. No. 4.6e-218;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464


RESULT 12
BD136154
LOCUS       BD136154               1518 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Vector.
ACCESSION   BD136154
VERSION     BD136154.1  GI:23231099
KEYWORDS    JP 2002507117-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1518)
  AUTHORS   Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: JP 2002507117-A 5 05-MAR-2002;
            OXFORD BIOMEDICA LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002507117-A/5
            PD   05-MAR-2002
            PF   04-JUN-1998 JP 1999501858
            PR   04-JUN-1997 GB    9711579.4,20-JUN-1997 GB    9713150.2 PR
            04-JUL-1997 GB    9714230.1
            PI   SUSAN MARY KINGSMAN,CHRISTOPHER ROBERT BEBBINGTON,FIONA  PI
            MARGARET ELLARD,
            PI   MILES WILLIAM CARROLL,KEVIN ALAN MYERS
            PC   C12N15/85,A61K48/00
            CC   Description of Artificial Sequence: DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .1518
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            99.3%;  Score 724.2;  DB 6;  Length 1518;
  Best Local Similarity  99.6%;  Pred. No. 5.3e-218;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206
```

```
Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 13
AX002782
LOCUS       AX002782               1518 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9855607.
ACCESSION   AX002782
VERSION     AX002782.1  GI:9885111
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bebbington,C.R., Carroll,M.W., Ellard,F.M., Kingsman,S.M. and
            Myers,K.A.
  TITLE     Vector
  JOURNAL   Patent: WO 9855607-A 5 10-DEC-1998;
            BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
            ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
            ALAN (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DNA"
ORIGIN

  Query Match             99.3%;  Score 724.2;  DB 6;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 5.3e-218;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 14
AX149550
LOCUS       AX149550               1518 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 11 from Patent WO0136486.
ACCESSION   AX149550
VERSION     AX149550.1  GI:14347988
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 11 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1518
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="B7-ScFv"
ORIGIN

  Query Match             99.3%;  Score 724.2;  DB 6;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 5.3e-218;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                |||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
                |||||||||
Db       1507 ATCAAACGG 1515


RESULT 15
AX149547
LOCUS       AX149547               1796 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 8 from Patent WO0136486.
ACCESSION   AX149547
VERSION     AX149547.1  GI:14347986
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kingsman,A.O., Kingsman,S.M., Bebbington,C.R., Carroll,M.W.,
            Ellard,F.M. and Myers,K.A.
  TITLE     Antibodies
  JOURNAL   Patent: WO 0136486-A 8 25-MAY-2001;
            Oxford Biomedica (UK) Limited (GB)
FEATURES             Location/Qualifiers
     source          1. .1796
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5T4ScFv.1-IgG"
ORIGIN

  Query Match            98.9%;  Score 721;  DB 6;  Length 1796;
  Best Local Similarity  99.3%;  Pred. No. 5.6e-217;
  Matches  724;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
                ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788

Qy        721 ATCAAACGG 729
                |||||||||
Db        789 ATCAAACGG 797


Search completed: March 14, 2005, 20:12:26
Job time : 3614 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 14:53:11 ; Search time 531 Seconds
(without alignments)
8127.103 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	728.2	99.9	729	2	AAV80290	Aav80290 Murine an
2	728.2	99.9	729	4	AAF89729	Aaf89729 Nucleotid
3	727.4	99.8	729	2	AAZ19786	Aaz19786 Anti-5T4
4	727.4	99.8	729	2	AAZ07810	Aaz07810 5T4 scFv
5	727.4	99.8	1807	2	AAV80291	Aav80291 Anti-5T4
6	724.4	99.4	1467	2	AAV80292	Aav80292 Human B7-
7	724.4	99.4	1467	4	AAF89730	Aaf89730 Nucleotid
8	724.2	99.3	1518	2	AAV80294	Aav80294 B7-1/scFv
9	724.2	99.3	1518	4	AAF89732	Aaf89732 Nucleotid
10	721	98.9	1796	4	AAF89733	Aaf89733 Nucleotid
11	721	98.9	2090	2	AAV80295	Aav80295 ScFv-IgE1
12	721	98.9	2090	4	AAF89734	Aaf89734 Nucleotid
13	463.6	63.6	804	13	ADR70322	Adr70322 Polioviru
14	446.8	61.3	852	12	ADF85425	Adf85425 V122scFv
15	442	60.6	1725	2	AAX01651	Aax01651 Bispecifi
16	439.4	60.3	759	2	AAV10378	Aav10378 Anti-CD86
17	438.8	60.2	864	2	AAV72072	Aav72072 Fusion pr
18	438.8	60.2	2019	2	AAV72059	Aav72059 Plasmid p
19	438.8	60.2	2025	2	AAV72064	Aav72064 Fusion pr
20	438.6	60.2	744	2	AAV11399	Aav11399 Human CD3
21	438.6	60.2	1668	2	AAX01652	Aax01652 Bispecifi
22	438.6	60.2	2438	12	ADO43004	Ado43004 DNA encod
23	438.2	60.1	828	10	ABT15854	Abt15854 Anti-huma
24	437.8	60.1	726	4	AAF30723	Aaf30723 Anti-FIX/
25	432.8	59.4	795	10	ABX13684	Abx13684 Mouse rec
26	432.8	59.4	810	13	ADR28056	Adr28056 Polynucle
27	430.8	59.1	2952	6	ABK13464	Abk13464 DNA encod
28	425.2	58.3	868	10	ACC57513	Acc57513 Newcastle
29	421.6	57.8	777	8	ABX12651	Abx12651 Venezuela
30	419.6	57.6	783	12	ADL65424	Adl65424 DNA gyras
31	418.4	57.4	774	6	AAS97138	Aas97138 P4-15 sin
32	417.6	57.3	744	2	AAX77247	Aax77247 Mouse scF
33	417.6	57.3	744	2	AAX77243	Aax77243 Mouse scF
34	417.2	57.2	720	10	ABT23322	Abt23322 VEGF bind
35	417.2	57.2	720	12	ADK18246	Adk18246 Mouse VEG
36	417.2	57.2	726	8	ACC83315	Acc83315 Single ch
37	417.2	57.2	726	13	ADT91208	Adt91208 Single ch
38	416.8	57.2	777	8	ABX12653	Abx12653 Venezuela
39	416.8	57.2	891	13	ADS20751	Ads20751 SBP tagge
40	415	56.9	876	4	AAF30734	Aaf30734 DNA encod
41	415	56.9	969	4	AAF30730	Aaf30730 Antibody
42	415	56.9	2190	4	AAF30729	Aaf30729 Antibody
43	413.4	56.7	716	10	ADC79233	Adc79233 VK-8-1.9
44	413	56.7	1920	10	ADH34695	Adh34695 CE7-speci
45	413	56.7	6834	10	ADH34699	Adh34699 CE7-speci

ALIGNMENTS

RESULT 1
AAV80290
ID AAV80290 standard; cDNA; 729 BP.
XX
AC AAV80290;
XX
DT 15-MAR-1999 (first entry)
XX
DE Murine anti-5T4 antigen monoclonal antibody scFv DNA.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; ss.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86002.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1A; 82pp; English.
XX
CC This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see
CC AAW86002), comprising the heavy chain variable region (VH) from the
CC murine 5T4 monoclonal antibody followed by a 15-amino acid flexible

```
CC   linker and the light chain variable region (VL) of the mouse 5T4
CC   antibody. The trophoblast cell surface antigen defined by monoclonal
CC   antibody 5T4 is expressed at high levels on the cells of a wide variety
CC   of human tumours. The 5T4scFv.1 DNA sequence can be used to construct
CC   single-chain antibodies (see AAV80291) and scFv fusion constructs (see
CC   AAV80292-96). The invention relates to a vector comprising a nucleotide
CC   sequence coding for a tumour interacting protein (TIP) and optionally a
CC   nucleotide sequence of interest (NOI) which encodes a protein of interest
CC   (POI), the vector being capable of delivering the NOI and/or POI to the
CC   tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC   vector is used to treat cancer, and may also used as a gene delivery
CC   system for introducing at least 1 gene encoding a TIP (preferably a
CC   tumour binding protein) into a haematopoietic cell lineage
XX
SQ   Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;

  Query Match             99.9%;  Score 728.2;  DB 2;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-197;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

```
RESULT 2
AAF89729
ID   AAF89729 standard; DNA; 729 BP.
XX
AC   AAF89729;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a 5T4 ScFv designated 5T4ScFv.1.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .729
FT                   /*tag=  a
FT                   /transl_except= (pos: 505. .507, aa: Ala)
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
DR   P-PSDB; AAB83835.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
XX
PS   Claim 7; Fig 1; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a 5T4 ScFv of the invention. The antibody comprises the VH and VL
CC   regions from murine 5T4 monoclonal antibody, joined by a linker sequence
XX
SQ   Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;

  Query Match             99.9%;  Score 728.2;  DB 4;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-197;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
```

```
Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

```
RESULT 3
AAZ19786
ID   AAZ19786 standard; DNA; 729 BP.
XX
AC   AAZ19786;
XX
DT   06-DEC-1999  (first entry)
XX
DE   Anti-5T4 secreted single chain antibody Fv fragment DNA.
XX
KW   Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
KW   nucleus; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .729
FT                   /*tag=  a
FT                   /product= "Anti-5T4 secreted single chain antibody Fv
FT                   fragment"
XX
PN   WO9945127-A2.
XX
PD   10-SEP-1999.
XX
PF   05-MAR-1999;   99WO-GB000674.
XX
PR   06-MAR-1998;   98GB-00004841.
PR   19-AUG-1998;   98GB-00018103.
PR   29-JAN-1999;   99GB-00002081.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Stratford IJ,  Patterson AV,  Kingsman SM,  Kan O,  Griffiths L;
PI   Mitrophanous K;
XX
DR   WPI; 1999-551046/46.
DR   P-PSDB; AAY42294.
XX
PT   New prodrug activating agent targeted to selected cells or tissues,
PT   particularly hypoxic cells, for treating e.g. tumors.
XX
PS   Example 9; Fig 3; 187pp; English.
XX
CC   This sequence represents an example of a DNA encoding a secreted single
CC   chain antibody Fv fragment, which is involved in transcellular
CC   localisation. In this example, the antibody is directed against the 5T4
CC   antigen. A secreted single chain antibody Fv fragment can be fused to
CC   cytochrome P450 reductase (P450R) derivatives such as anchorless P450R
CC   (AAY42287) or FN fragment (AAY42288). This enables the fusion protein to
CC   be delivered to other cells where it is then transported to the nucleus.
CC   Many drugs' sites of action are in the nucleus, rather than the
CC   cytoplasm, where P450R normally functions. P450R or its derivatives can
CC   be used to activate prodrugs to their active form via reduction.
CC   Administration of a prodrug is useful where the active drug may be
CC   metabolised before it reaches its site of action or where the active drug
CC   is cytotoxic, e.g., anticancer drugs. Targetted delivery of such prodrug
CC   activators allows a reduction in dose of the prodrug, and thus of
CC   systemic side-effects. P450R derivative fusion proteins, or vectors that
CC   express them, are specifically used to treat tumours, inflammation,
CC   atherosclerosis and muscular dystrophy, but may also be used to treat
CC   many other conditions, e.g., cerebral malaria, rheumatoid arthritis, or
CC   conditions associated with hypoxia, ischaemia or hypoglycemia, or to
CC   deliver antibiotics, antiviral agents, analgesics, anaesthetics, anti-
CC   inflammatories, antineoplastic agents and diagnostic agents
XX
SQ   Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;
```

```
  Query Match             99.8%;  Score 727.4;  DB 2;  Length 729;
  Best Local Similarity   99.9%;  Pred. No. 3.6e-197;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
```

```
Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 4
AAZ07810
ID AAZ07810 standard; DNA; 729 BP.
XX
AC AAZ07810;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody encoding DNA.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
KW 5T4 scFv; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .729
FT /*tag= a
XX
PN WO9945126-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB000672.
XX
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
DR P-PSDB; AAY27407.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
XX
PS Example 9; Fig 3F; 149pp; English.
XX
CC The invention provides a new prodrug activating agent that comprises: (i)
CC a localization domain (LD; other than a tumor-selective antibody) and a
CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (iii) a modified hematopoietic
CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (ii). The prodrug activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of prodrug, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively in
CC hypoxic cells. The present sequence represents the DNA encoding the
CC single chain variable antibody fragment against the tumor antigen 5T4
CC (5T4 scFv). 5T4 scFv is used in the construction of a fusion protein
CC comprising 5T4 scFv and a human P450 reductase derivative alP450R
XX
SQ Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;

Query Match 99.8%; Score 727.4; DB 2; Length 729;
Best Local Similarity 99.9%; Pred. No. 3.6e-197;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
```

```
Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729
```

RESULT 5
AAV80291
ID AAV80291 standard; cDNA; 1807 BP.
XX
AC AAV80291;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-5T4 single chain antibody 5T4Sab1 DNA.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sab1; ss.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 3. .1790
FT /*tag= a
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86003.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 1; Fig 1B; 82pp; English.
XX
CC This DNA sequence encodes a single chain antibody (Sab), termed 5T4Sab1
CC (see AAW86003), comprising an scFv derived from murine monoclonal
CC antibody 5T4 (see AAW86002) and the human g1 constant region. It was
CC constructed from cassettes comprising a translation initiation signal and
CC signal peptide (see AAV80297), the sequence of the secreted portion of
CC 5T4scFv.1, and the sequence of the human g1 constant region genomic
CC clone. The trophoblast cell surface antigen defined by 5T4 is expressed
CC at high levels on the cells of a wide variety of human tumours. The
CC invention relates to a vector comprising a nucleotide sequence coding for
CC a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC of interest (NOI) which encodes a protein of interest (POI), the vector
CC being capable of delivering the NOI and/or POI to the tumour recognised
CC by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC treat cancer, and may also used as a gene delivery system for introducing
CC at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage
XX
SQ Sequence 1807 BP; 432 A; 543 C; 469 G; 363 T; 0 U; 0 Other;

Query Match 99.8%; Score 727.4; DB 2; Length 1807;
Best Local Similarity 99.9%; Pred. No. 4.9e-197;
Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 6
AAV80292
ID AAV80292 standard; cDNA; 1467 BP.
XX
AC AAV80292;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human B7-1.5T4.1 gene fusion, specific for human 5T4.
XX
KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW monoclonal antibody; single chain antibody; scFv; mouse; human; B7-1;
KW co-stimulatory molecule; ss.
XX
OS Mus sp.
OS Homo sapiens.

OS Synthetic.
OS Chimeric.
XX
PN WO9855607-A2.
XX
PD 10-DEC-1998.
XX
PF 04-JUN-1998; 98WO-GB001627.
XX
PR 04-JUN-1997; 97GB-00011579.
PR 20-JUN-1997; 97GB-00013150.
PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX
DR WPI; 1999-059910/05.
DR P-PSDB; AAW86004.
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
PS Example 5; Fig 2; 82pp; English.
XX
CC This DNA sequence encodes B7-1.5T4.1 (see AAW86004), a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human co-
CC stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. The cDNA can
CC be inserted into vector pCI to allow expression of the fusion protein in
CC mammalian cells. The trophoblast cell surface antigen defined by 5T4 is
CC expressed at high levels on the cells of a wide variety of human tumours.
CC The invention relates to a vector comprising a nucleotide sequence coding
CC for a tumour interacting protein (TIP) and optionally a nucleotide
CC sequence of interest (NOI) which encodes a protein of interest (POI), the
CC vector being capable of delivering the NOI and/or POI to the tumour
CC recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is
CC used to treat cancer, and may also used as a gene delivery system for
CC introducing at least 1 gene encoding a TIP (preferably a tumour binding
CC protein) into a haematopoietic cell lineage. B7-1 is expected to bind
CC specifically to CD28 and CTLA-4 present on human T-cells
XX
SQ Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;

Query Match 99.4%; Score 724.4; DB 2; Length 1467;
Best Local Similarity 99.9%; Pred. No. 3.3e-196;
Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

RESULT 7
AAF89730
ID AAF89730 standard; DNA; 1467 BP.
XX
AC AAF89730;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a B7-1.5T4.1 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1467
FT /*tag= a
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR P-PSDB; AAB83836.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a

```
PT   disease condition associated with disease associated molecule.
XX
PS   Claim 8; Fig 2; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a B7-1.5T4.1 fusion protein. This comprises the N-terminus of the
CC   5T4 ScFv is fused after amino acid 215 of human B7-1
XX
SQ   Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;

  Query Match             99.4%;  Score 724.4;  DB 4;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 3.3e-196;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464


RESULT 8
AAV80294
ID   AAV80294 standard; cDNA; 1518 BP.
XX
AC   AAV80294;
XX
DT   17-OCT-2003  (revised)
DT   15-MAR-1999  (first entry)
XX
DE   B7-1/scFv specific for use in cancer gene therapy.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; scFv; mouse; B7-1;
KW   co-stimulatory molecule; ss.
XX
OS   Mus sp.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 10; Page 63-64; 82pp; English.
XX
CC   This DNA sequence encodes a fusion protein comprising the extracellular
CC   domain of mouse co-stimulatory molecule B7-1 joined via a flexible
CC   peptide linker to an scFv (see AAW86002) derived from murine 5T4
CC   monoclonal antibody. The fusion can be used to construct a recombinant
CC   vector, e.g. retrovirus, lentivirus, adenovirus, poxvirus, vaccinia virus
CC   or baculovirus, used for direct treatment of tumour patients. The
CC   trophoblast cell surface antigen defined by 5T4 is expressed at high
CC   levels on the cells of a wide variety of human tumours. The invention
CC   relates to a vector comprising a nucleotide sequence coding for a tumour
CC   interacting protein (TIP) and optionally a nucleotide sequence of
CC   interest (NOI) which encodes a protein of interest (POI), the vector
CC   being capable of delivering the NOI and/or POI to the tumour recognised
CC   by the TIP. Delivery can be in vivo or ex vivo. The vector is used to
CC   treat cancer, and may also used as a gene delivery system for introducing
CC   at least 1 gene encoding a TIP (preferably a tumour binding protein) into
CC   a haematopoietic cell lineage. B7-1 binds specifically to CD28 and CTLA-4
CC   present on human CD4 and CD8 cells. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

  Query Match             99.3%;  Score 724.2;  DB 2;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 3.8e-196;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846
```

```
Qy          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
               |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy         361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy         421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy         481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
               |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy         541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy         601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy         661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy         721 ATCAAACGG 729
               |||||||||
Db        1507 ATCAAACGG 1515
```

RESULT 9
AAF89732
ID AAF89732 standard; DNA; 1518 BP.
XX
AC AAF89732;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a B7 link ScFv sequence.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Example 8; Fig 5; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes a B7 link ScFv sequence. A human B7 sequence is linked to a ScFv
CC of the invention
XX
SQ Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;

Query Match 99.3%; Score 724.2; DB 4; Length 1518;
Best Local Similarity 99.6%; Pred. No. 3.8e-196;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy           1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy          61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy         121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy         181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy         241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy         301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
               |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy         361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy         421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy         481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
```

```
                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
                |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 10
AAF89733
ID AAF89733 standard; DNA; 1796 BP.
XX
AC AAF89733;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of an Ig-5T4 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder; ss.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 12. .1790
FT /*tag= a
FT /transl_except= (1518. .1520, aa: Met)
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR P-PSDB; AAB83838.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX
PS Claim 9; Fig 6; 118pp; English.
XX
CC The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC encodes an Ig-5T4 fusion protein
XX
SQ Sequence 1796 BP; 429 A; 539 C; 466 G; 362 T; 0 U; 0 Other;

Query Match 98.9%; Score 721; DB 4; Length 1796;
Best Local Similarity 99.3%; Pred. No. 3.3e-195;
Matches 724; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 11
AAV80295
ID AAV80295 standard; cDNA; 2090 BP.
XX
AC AAV80295;

```
XX
DT   15-MAR-1999  (first entry)
XX
DE   ScFv-IgE1 fusion construct for use in cancer gene therapy.
XX
KW   Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW   monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
PN   WO9855607-A2.
XX
PD   10-DEC-1998.
XX
PF   04-JUN-1998;   98WO-GB001627.
XX
PR   04-JUN-1997;   97GB-00011579.
PR   20-JUN-1997;   97GB-00013150.
PR   04-JUL-1997;   97GB-00014230.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman SM,  Bebbington CR,  Ellard FM,  Carroll MW,  Myers KA;
XX
DR   WPI; 1999-059910/05.
XX
PT   New vector encoding a tumour interacting protein for treating cancer -
PT   contains a desired nucleotide sequence and/or protein which recognises
PT   tumours, and is used as a gene delivery system to treat cancer.
XX
PS   Example 13; Page 64; 82pp; English.
XX
CC   This DNA sequence encodes a fusion protein comprising the human IgE1
CC   heavy constant region joined via a flexible peptide linker to an scFv
CC   (see AAW86002) derived from murine 5T4 monoclonal antibody. The fusion
CC   construct can be incorporated into a recombinant viral vector for use in
CC   gene therapy of cancer. The trophoblast cell surface antigen defined by
CC   5T4 is expressed at high levels on the cells of a wide variety of human
CC   tumours. Binding of IgE to tumour cells should promote a strong histamine
CC   and hence inflammatory response and destruction of tumour cells. The
CC   invention relates to a vector comprising a nucleotide sequence coding for
CC   a tumour interacting protein (TIP) and optionally a nucleotide sequence
CC   of interest (NOI) which encodes a protein of interest (POI), the vector
CC   being capable of delivering the NOI and/or POI to the tumour recognised
CC   by the TIP. Delivery can be in vivo or ex vivo
XX
SQ   Sequence 2090 BP; 461 A; 653 C; 565 G; 411 T; 0 U; 0 Other;

  Query Match            98.9%;  Score 721;  DB 2;  Length 2090;
  Best Local Similarity  99.3%;  Pred. No. 3.5e-195;
  Matches  724;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 12
AAF89734
ID   AAF89734 standard; DNA; 2090 BP.
XX
AC   AAF89734;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Nucleotide sequence of a SvFv-IgE protein.
XX
KW   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW   hypersensitivity; autoimmune disease; central nervous system disorder;
KW   Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW   cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW   Helicobacter-related disease; immune disorder; ss.
XX
OS   Synthetic.
XX
PN   WO200136486-A2.
XX
PD   25-MAY-2001.
XX
PF   13-NOV-2000; 2000WO-GB004317.
XX
PR   18-NOV-1999;   99WO-GB003859.
PR   15-FEB-2000; 2000GB-00003527.
PR   02-MAR-2000; 2000GB-00005071.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   Kingsman A,  Kingsman SM,  Bebbington CR,  Carroll MW,  Ellard FM;
PI   Myers KA;
XX
DR   WPI; 2001-343805/36.
XX
PT   Use of single chain antibody capable of recognizing a disease associated
PT   molecule for manufacturing a medicament for preventing and/or treating a
PT   disease condition associated with disease associated molecule.
```

```
XX
PS   Example 11; Fig 7; 118pp; English.
XX
CC   The specification describes the use of a single chain antibody (ScFv),
CC   which is capable of recognizing a disease associated molecule in the
CC   manufacture of a medicament for the prevention and treatment of a disease
CC   condition. The ScFv antibody is useful in the manufacture of a
CC   medicament, for affecting a disease in vivo, for preparing a
CC   pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC   treatment of a disease. The ScFv antibody is also useful for treating
CC   inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC   diseases, cancers, central nervous system disorders including Parkinson's
CC   disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC   diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC   related diseases, and other immune disorders. The present sequence
CC   encodes a ScFv of the invention linked to an IgE sequence
XX
SQ   Sequence 2090 BP; 461 A; 654 C; 564 G; 411 T; 0 U; 0 Other;

  Query Match             98.9%;  Score 721;  DB 4;  Length 2090;
  Best Local Similarity   99.3%;  Pred. No. 3.5e-195;
  Matches  724;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 13
ADR70322
ID   ADR70322 standard; DNA; 804 BP.
XX
AC   ADR70322;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Poliovirus receptor (PVR)-specific scF2 coding sequence.
XX
KW   poliovirus receptor; PVR; CD155; cluster of differentiation 155;
KW   receptor mediated adhesion modulation;
KW   cell trafficking behaviour modulation;
KW   cell invasion behaviour modulation; proliferative disorder; cancer;
KW   metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;
KW   scFv2; gene; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .804
FT                   /*tag=  a
FT                   /partial
FT                   /product= "PVR-specific scFv2 protein"
FT                   /note= "No start codon is given"
XX
PN   WO2004074324-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-EP001637.
XX
PR   24-FEB-2003; 2003US-0450064P.
PR   28-MAY-2003; 2003EP-00012314.
XX
PA   (XERI-) XERION PHARM AG.
PA   (TUFT ) UNIV TUFTS.
XX
PI   Unger CM,  Beste G,  Zehetmeier C,  Lain B,  Torella C,  Jay DG;
PI   Eustace BK,  Sloan KE;
XX
DR   WPI; 2004-652917/63.
DR   P-PSDB; ADR70320.
XX
PT   New molecules that modulate poliovirus receptor (PVR) mediated adhesion,
PT   trafficking and/or invasion behavior of a cell expressing CD155 or PVR,
PT   useful for preventing or treating proliferative disorders, such as
PT   cancer.
XX
PS   Claim 8; SEQ ID NO 6; 87pp; English.
XX
CC   The invention comprises molecules that specifically bind to at least one
CC   intra- or extracellular domain of the poliovirus receptor (PVR) - also
CC   known as CD155 (cluster of differentiation 155). The molecules of the
CC   invention have the ability to modulate receptor mediated adhesion,
CC   trafficking and/or invasion behaviour of a cell expressing PVR. The
CC   molecules of the invention are useful for the prevention and/or treatment
CC   of proliferative disorders, cancer or metastasis. The molecules of the
CC   invention are also useful for identifying agents that can modulate PVR-
CC   mediated adhesion or invasion potential of cells. The present DNA
CC   sequence encodes a PVR-specific scFv protein of the invention.
XX
SQ   Sequence 804 BP; 213 A; 197 C; 227 G; 167 T; 0 U; 0 Other;

  Query Match             63.6%;  Score 463.6;  DB 13;  Length 804;
  Best Local Similarity   79.8%;  Pred. No. 7.5e-122;
  Matches  579;  Conservative    0;  Mismatches  129;  Indels   18;  Gaps    2;

Qy          7 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 66
              ||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||
```

```
Db          1 CAGCTGCAGCAGTCTGGACCTGAGTTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 60

Qy         67 AAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGA 126
              ||| ||||||| ||| | |||||||  |||  ||||||||||||||| ||||||||||||
Db         61 AAGACTTCTGGATACACGTTCACTGAATACACCATGCACTGGGTGAAACAGAGCCATGGA 120

Qy        127 AAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAG 186
              |||||||||||||||||||| ||||| |||||||||||||| ||||  ||||||||||
Db        121 AAGAGCCTTGAGTGGATTGGAGGTATTCATCCTAACAATGGTGATACTAGCTACAACCAG 180

Qy        187 AAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAG 246
              |  |||||||  ||||||| ||| ||||||||||||||||||| ||||||||||||||||
Db        181 AGGTTCAAGGGAAAGGCCACATTGACTGTAGACAAGTCATCCAGCACAGCCTACATGGAG 240

Qy        247 CTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATT 306
              |||||||||||  |||||||||||  |||||  ||||||||||||||||||||  ||   |
Db        241 CTCCGCAGCCTAACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGATGGACGGGG--- 297

Qy        307 ACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGT 366
                      |   | ||||||||||| ||||  ||| |  |||| || ||  |||||||
Db        298 ---------GACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTGTCGACAGGTGGA 348

Qy        367 GGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCT------AGTATTGTGATGACC 420
              || ||    || || || ||| ||||||| ||||||  |         ||||||||||
Db        349 GGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGAAGTGCACTCGACATTGTGATGACA 408

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||| |||| | |||| ||      |||| ||||||||||| | | | ||||||||||||
Db        409 CAGTCTCCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCC 468

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||| | |||| ||| | ||||||  ||||| ||||||| |||||||| |||||||  |
Db        469 AGTCAAAATGTGGGTACTAATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAA 528

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                 || || | ||   |||||   || |||  ||||||||||||||||||||  ||||||
Db        529 GCACTGATTTACTCGGCATCCTACCGGTACAGTGGAGTCCCTGATCGCTTCACAGGCAGT 588

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              |||| |||||| |||||||| |||||||||||  | |||||  |||||||| ||||||
Db        589 GGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGAAGACTTGGCAGAG 648

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              |||||||||||||| || | |  | |||    |||||||| || || ||||||||||||
Db        649 TATTTCTGTCAGCAATATAACAGCTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAA 708

Qy        721 ATCAAA 726
              || |||
Db        709 ATAAAA 714


RESULT 14
ADF85425
ID   ADF85425 standard; DNA; 852 BP.
XX
AC   ADF85425;
XX
DT   26-FEB-2004  (first entry)
XX
DE   V122scFv clone encoding sequence.
XX
KW   Fv library; ds.
XX
OS   Unidentified.
XX
PN   JP2003334075-A.
XX
PD   25-NOV-2003.
XX
PF   21-MAY-2002; 2002JP-00145858.
XX
PR   21-MAY-2002; 2002JP-00145858.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2004-027982/03.
DR   P-PSDB; ADF85426.
XX
PT   Mutated Fv library useful for screening mutated Fv for preparation of
PT   mutated antibody for diagnostic purposes, having mutations at specific
PT   amino acid positions of complementarity determining regions of antibody.
XX
PS   Disclosure; SEQ ID NO 1; 17pp; Japanese.
XX
CC   The present invention relates to mutated Fv library having mutations
CC   designed such that the amino acid at position k (k is integer 2&le;k&le;
CC   20) is introduced at amino acid position m (m is integer 2&le;m&le;(n-1))
CC   chosen from a region consisting of n residues (n is integer 3&le;n
CC   contained in complementarity determining regions (CDR) or other closer
CC   regions of an antibody, and forms limited Fv repertory of ( n )C m &times
CC   ;km. The invention can be used for efficiently acquiring mutated
CC   antibody. The present sequence represents V122scFv clone encoding
CC   sequence.
XX
SQ   Sequence 852 BP; 208 A; 222 C; 229 G; 193 T; 0 U; 0 Other;

  Query Match           61.3%;  Score 446.8;  DB 12;  Length 852;
  Best Local Similarity   77.3%;  Pred. No. 4.8e-117;
  Matches  563;  Conservative    0;  Mismatches  147;  Indels   18;  Gaps    1;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||  | || |||||||| |||||| |||||||||||||||||||||||||||||| |
Db         68 AGGTGAAACTGCAGCAGTCAGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGT 127

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||||||||| ||| |||||||| ||||    ||||||||||||||||||  |
Db        128 CCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATGCACTGGGTGAAGCAGAAGC 187

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||  || ||||||||||||||||  | |||||||| |||||| || || |  |||||
Db        188 CTGGGCAGGGCCTTGAGTGGATTGGATATGTTAATCCTTACAATGATGGTATTAACTACA 247

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |  |||| ||||| | |||||||| | | |||  ||||||  || |||| ||||||||||
Db        248 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 307

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              |||||||| |||||||||  ||||| ||||||||||||||||||||||||||||||
Db        308 TGGAGCTCAGCAGCCTGACCTCTGACGACTCTGCGGTCTATTACTGTGCAAGA------- 360

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                    | | | ||||||| ||||| |||  ||| | ||||||||||||||||||
Db        361 -----------AAGGGTTTGGACTATTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 409

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || |      || || || ||| ||||||| ||||||||     || | | | || |
Db        410 GTGGAGGCGCTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 469

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| | |||| ||      |||| |||||||||||| | | | ||||||||||||
Db        470 AGTCTCCAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCA 529

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  |||| ||| | ||||||  ||||| |||||||| ||||| || ||||||| |
Db        530 GTCAGTTTGTGGGTACTTATGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAAG 589

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
                || || | ||   ||||||  ||   | ||||||||||||||||||||  |||||||
Db        590 CACTGATTTACTCGGCATCCACCCGGCGCACTGGAGTCCCTGATCGCTTCACAGGCAGTG 649

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| |||||| |||||||| ||||||| |||| | ||||| ||||||| ||||||  |
Db        650 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGAGT 709

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||| ||||| |    | |||||    ||||||||    ||||||||||||||||
```

```
Db        710 ATTTCTGTGAGCAATACAGCAGCTCTCCGTATACGTTCGGATCGGGCACCAAGCTGGAAA 769

Qy        722 TCAAACGG 729
              ||||||||
Db        770 TCAAACGG 777


RESULT 15
AAX01651
ID   AAX01651 standard; DNA; 1725 BP.
XX
AC   AAX01651;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Bispecific tetravalent antibody BiTAbB724-IG10H6 DNA.
XX
KW   B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
KW   T cell activation; inhibitor; graft versus host disease;
KW   transplant rejection; allograft rejection; autoimmune disease; allergy;
KW   therapy; human; bispecific tetravalent antibody; BiTAb;
KW   BiTAbB7-24-1G10H6; ss.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1726
FT                   /*tag=  a
FT                   /transl_except= (pos:780. .782, aa:Ile)
FT                   /transl_except= (pos:967. .969, aa:Xaa)
FT                   /note= "Xaa= Gln-Leu-Val-Gln-Val-Gln"
FT   sig_peptide     1. .72
FT                   /*tag=  b
FT                   /note= "pelB signal sequence"
FT   mat_peptide     73. .1726
FT                   /*tag=  c
XX
PN   WO9858965-A2.
XX
PD   30-DEC-1998.
XX
PF   22-JUN-1998;   98WO-EP003791.
XX
PR   20-JUN-1997;   97EP-00870092.
XX
PA   (INNO-) INNOGENETICS NV.
XX
PI   Lorre K,  Sablon E,  Buyse M,  Bosman A;
XX
DR   WPI; 1999-105615/09.
DR   P-PSDB; AAW90217.
XX
PT   New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT   immune diseases including allograft rejection.
XX
PS   Example 7.1; Fig 15; 182pp; English.
XX
CC   This DNA sequence encodes the bispecific tetravalent antibody BiTAbB7-24-
CC   1G10H6 (see AAW90217) comprising the anti-B7.1 murine monoclonal antibody
CC   (MAb) B7-24 VH region joined, via a flexible synthetic linker, to the B7-
CC   24 VL region, the human IgG3 hinge region, a helix-turn-helix
CC   dimerisation domain, the human IgG3 hinge domain, the anti-B7.2 MAb 1G10
CC   VH region, another flexible linker, the 1G10 VL region and a
CC   hexahistidine tag. The BiTAb has been expressed in Escherichia coli
CC   cells. It cross-links, and/or cross-reacts, with the costimulatory
CC   molecules B7.1 and B7.2 expressed on the membrane of professional antigen
CC   -presenting cells, leading to the inhibition of antigen-specific T cell
CC   activation. The invention relates to such B7-binding molecules, methods
CC   for their production, and their use for treating or preventing diseases
CC   of the immune system, in particular graft rejection, graft versus host
CC   disease, allergy and autoimmune diseases (claimed)
XX
SQ   Sequence 1725 BP; 424 A; 439 C; 468 G; 394 T; 0 U; 0 Other;

  Query Match             60.6%;  Score 442;  DB 2;  Length 1725;
  Best Local Similarity   78.5%;  Pred. No. 1.4e-115;
  Matches  590;  Conservative    0;  Mismatches  135;  Indels   27;  Gaps    4;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||  | || |||||||||||||||||| |||| |||||||||| ||||||||||||||||
Db        959 AGGTGAAACTGCAGCAGTCTGGACCTGAGCTGGAGAAGCCTGGCGCTTCAGTGAAGATAT 1018

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||||||||||||||||||||||||| || ||||| ||||||||||||||||||
Db       1019 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCCACAACATGAACTGGGTGAAGCAGAGCA 1078

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||||||||||||||||||||||||  |||| ||||  || |||||| |||| |||||
Db       1079 ATGGAAAGAGCCTTGAGTGGATTGGAATTATTGATCCCTACTATGGTGGTACTAGCTACA 1138

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              ||| ||| ||| ||| |||||||| ||| |||||||||| || |||| ||||||||||
Db       1139 ACCCGAAGTTCGAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTACA 1198

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAT----CT 297
              || |||||   |||||||||| |||||||||| |||||||||||||||||||    ||
Db       1199 TGCAGCTCGAGAGCCTGACATCCGAGGACTCTGCAGTCTATTACTGTGCAAGATTCGCCT 1258

Qy        298 ACTATGATTACGA--ACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCT 355
              |||||| | || |  | ||| |||||||||||||||| ||||  ||| | ||||||||||
Db       1259 ACTATGGTGACTACTATTATATTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCT 1318

Qy        356 CCTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGA 415
              |||||||||| || ||    || || || ||| |||||||| ||||||||    || | ||
Db       1319 CCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGC 1378

Qy        416 TGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCA 475
              | || ||| |||| ||| ||| ||| || ||||||||   ||| || || ||||| |
Db       1379 TCACTCAGTCTCCATCATCTCTGGCTGTGTCTGCAGGAGAAGAGGTCACTATGACCTGTA 1438

Qy        476 AGGCCAGTCAGAGTGT-----------------GAGTAATGATGTAGDTTGGTACCAAC 517
              || ||||||| |||||                 ||  ||  |  | |  ||||||||||
Db       1439 AGTCCAGTCAAAGTGTTTTATACAGTTCAAATCAGAAGAACTACTTGGCCTGGTACCAAC 1498

Qy        518 AGAAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAG 577
              |||| |||||||||||||||| | |||| || | ||    |||||| | |  |  | || |
Db       1499 AGAAACCAGGGCAGTCTCCTAAATTGCTGATCTACTGGGCATCCACTAGGGAATCAGGTG 1558

Qy        578 TCCCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTT 637
              ||||||||||||||   |||||||||| |||||| |||||  || | |||||||||| |
Db       1559 TCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTTTCTCTTACCATCAGCAGTG 1618

Qy        638 TGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGT 697
              | || ||||| |||||||||||||||| |||||| |||   ||    ||  |  |||||
Db       1619 TACAAGCTGAGGACCTGGCAGTTTATTACTGTCATCAA---TACCTCTCCTCGTGGACGT 1675

Qy        698 TCGGTGGAGGCACCAAGCTGGAAATCAAACGG 729
              |||||||||| |||||||||||||| ||||||
Db       1676 TCGGTGGAGGTACCAAGCTGGAAATAAAACGG 1707


Search completed: March 14, 2005, 19:12:12
Job time : 538 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:41:00 ; Search time 190 Seconds
(without alignments)
6278.135 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	458.2	62.9	756	2	US-08-797-689-17	Sequence 17, Appl
2	458.2	62.9	756	4	US-09-984-186-17	Sequence 17, Appl
3	438.8	60.2	864	3	US-09-423-439-47	Sequence 47, Appl
4	438.8	60.2	2019	3	US-09-423-439-31	Sequence 31, Appl
5	438.8	60.2	2025	3	US-09-423-439-37	Sequence 37, Appl
6	421.6	57.8	777	4	US-10-092-246-5	Sequence 5, Appli
7	421.6	57.8	777	4	US-10-096-246A-5	Sequence 5, Appli
8	416.8	57.2	777	4	US-10-092-246-7	Sequence 7, Appli
9	416.8	57.2	777	4	US-10-096-246A-7	Sequence 7, Appli
10	413.8	56.8	723	4	US-09-581-345-1	Sequence 1, Appli
11	412	56.5	777	4	US-10-092-246-6	Sequence 6, Appli
12	412	56.5	777	4	US-10-096-246A-6	Sequence 6, Appli
13	410.8	56.4	717	3	US-09-142-974B-1	Sequence 1, Appli
14	410.8	56.4	1176	3	US-09-142-974B-3	Sequence 3, Appli
15	400.2	54.9	777	4	US-10-092-246-4	Sequence 4, Appli
16	400.2	54.9	777	4	US-10-096-246A-4	Sequence 4, Appli
17	399.2	54.8	774	4	US-10-092-246-3	Sequence 3, Appli
18	399.2	54.8	774	4	US-10-096-246A-3	Sequence 3, Appli
19	394.4	54.1	774	4	US-10-092-246-1	Sequence 1, Appli
20	394.4	54.1	774	4	US-10-096-246A-1	Sequence 1, Appli
21	394	54.0	726	2	US-08-553-497A-25	Sequence 25, Appl
22	391.8	53.7	726	2	US-08-553-497A-27	Sequence 27, Appl
23	391.8	53.7	732	2	US-08-553-497A-19	Sequence 19, Appl
24	388.6	53.3	732	2	US-08-553-497A-21	Sequence 21, Appl
25	388.2	53.3	1135	4	US-09-203-958A-3	Sequence 3, Appli
26	386.6	53.0	894	4	US-09-486-814A-1	Sequence 1, Appli
27	383.6	52.6	719	3	US-08-279-772A-7	Sequence 7, Appli
28	383.6	52.6	720	3	US-08-902-486-10	Sequence 10, Appl
29	382.2	52.4	717	4	US-09-473-653-5	Sequence 5, Appli
30	382	52.4	1797	1	US-08-463-163-2	Sequence 2, Appli
31	379.6	52.1	771	4	US-09-526-738A-1	Sequence 1, Appli
32	379.6	52.1	780	4	US-09-526-738A-3	Sequence 3, Appli
33	379.4	52.0	843	3	US-09-423-439-43	Sequence 43, Appl
34	379.4	52.0	1998	3	US-09-423-439-50	Sequence 50, Appl
35	378.4	51.9	831	2	US-08-403-853-17	Sequence 17, Appl
36	377.4	51.8	738	2	US-08-553-497A-23	Sequence 23, Appl
37	376.2	51.6	2012	1	US-08-235-838-15	Sequence 15, Appl
38	376.2	51.6	2012	2	US-08-465-473B-15	Sequence 15, Appl
39	374.4	51.4	748	1	US-08-235-838-10	Sequence 10, Appl
40	374.4	51.4	748	2	US-08-465-473B-10	Sequence 10, Appl
41	373.6	51.2	810	2	US-08-652-507-1	Sequence 1, Appli
42	371.4	50.9	720	2	US-08-800-198-7	Sequence 7, Appli
43	371.4	50.9	720	3	US-09-296-595-7	Sequence 7, Appli
44	371.4	50.9	1679	2	US-08-661-052-15	Sequence 15, Appl
45	371.4	50.9	1679	3	US-09-188-082-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-797-689-17
; Sequence 17, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

```
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..752
US-08-797-689-17

  Query Match             62.9%;  Score 458.2;  DB 2;  Length 756;
  Best Local Similarity   77.6%;  Pred. No. 3.5e-136;
  Matches  572;  Conservative    0;  Mismatches  153;  Indels   12;  Gaps    1;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              |||| |||||  |||||||||||||||| |||||||||||||||||| |||||||||||  |
Db         13 AGGTGCAGCTCGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATTT 72

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              ||||||| |||||||| ||| |||||| | | |   |  ||| ||||||||||||||| |
Db         73 CCTGCAAAGCTTCTGGCTACGCATTCAGTAGGTCTTGGATGAACTGGGTGAAGCAGAGGC 132

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
               |||| || | |||||||||||||||||| ||| |||||    |||| | |||    ||||
Db        133 CTGGACAGGGTCTTGAGTGGATTGGACGGATTTATCCTGGAGATGGAGATACCAAATACA 192

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |   ||| ||||||| |||||||| | | ||||  ||||  ||||||| ||||||||||
Db        193 ATGGGAAGTTCAAGGGCAAGGCCACACTGACTGCGGACAGATCATCCAGCACAGCCTACA 252

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||| |||| || |||||||||||||| |||||||| |    | |
Db        253 TGCAGCTCAGCAGCCTGACCTCTGTGGGCTCTGCGGTCTATTTCTGTGCAAAAGAGAACA 312

Qy        302 ------------TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCA 349
                          ||    |||||| |||||||||||||| ||||  ||| | ||||
Db        313 ATAGGTTCGACGAGAGGGGTTACTATGCTATGGACTACTGGGGCCAAGGGACCACGGTCA 372

Qy        350 CCGTCTCCTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTA 409
              |||||||||||||||| |||||    || ||||| ||  | || ||||||||||||  |
Db        373 CCGTCTCCTCAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTAACA 432

Qy        410 TTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAA 469
              ||  | |||||||| |||| |  | | ||      |||| |||||||||||| | ||| |
Db        433 TTCAGTTGACCCAGTCTCCAAATTCCATGTCCACATCAGTAGGAGACAGGGTCAGCATCA 492

Qy        470 CCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGC 529
              ||||||||||||||||  |||| || |  |||||  ||||| |||||||| |||||||
Db        493 CCTGCAAGGCCAGTCAGGATGTGGATACTTCTGTAGCCTGGTATCAACAGAAACCAGGGC 552

Qy        530 AGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCT 589
              | ||||||| ||| || || | ||   ||||||  ||  || ||||||||||||||||||
Db        553 AATCTCCTAAACTACTGATTTACTGGGCATCCACCCGGCACACTGGAGTCCCTGATCGCT 612

Qy        590 TCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAG 649
              |||  |||||||||| |||||| |||||||| ||||||| |||| | |||||  ||||||
Db        613 TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAG 672

Qy        650 ACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCA 709
              ||  ||||| |||||||||||||||| ||   |  | |||   |||||||||||||| |
Db        673 ACTCGGCAGATTATTTCTGTCAGCAATATAGCAGCTATCCGTGGACGTTCGGTGGAGGGA 732

Qy        710 CCAAGCTGGAAATCAAA 726
              |||||||||| ||||||
Db        733 CCAAGCTGGAGATCAAA 749


RESULT 2
US-09-984-186-17
; Sequence 17, Application US/09984186
; Patent No. 6686179
;   GENERAL INFORMATION:
;        APPLICANT: Fleer, Reinhard
;                   Fournier, Alain
;                   Guitton, Jean-Dominique
;                   Jung, Gerard
;                   Yeh, Patrice
;        TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;                            PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;                            CONTAINING SAID POLYPEPTIDES
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;             STREET: 500 Arcola Road, 3C43
;             CITY: Collegeville
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 19426
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Macintosh
;             OPERATING SYSTEM: System 7.1
;             SOFTWARE: Word 5.1 (PatentIn)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/984,186
;             FILING DATE: 29-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/797,689
;             FILING DATE: 31-JAN-1997
;             APPLICATION NUMBER: US 08/256,927
;             FILING DATE: 28-JUL-1994
;             APPLICATION NUMBER: FR 92/01064
;             FILING DATE: 31-JAN-1992
;             APPLICATION NUMBER: PCT/FR93/00085
;             FILING DATE: 28-JAN-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith Ph.D., Julie K.
;             REGISTRATION NUMBER: P-38,619
;             REFERENCE/DOCKET NUMBER: ST92006-US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (610) 454-3839
;             TELEFAX: (610) 454-3808
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  3..752
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-984-186-17

  Query Match             62.9%;  Score 458.2;  DB 4;  Length 756;
  Best Local Similarity   77.6%;  Pred. No. 3.5e-136;
  Matches  572;  Conservative    0;  Mismatches  153;  Indels   12;  Gaps    1;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              |||| |||||  |||||||||||||||| |||||||||||||||||| |||||||||||  |
Db         13 AGGTGCAGCTCGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATTT 72

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              ||||||| |||||||| ||| |||||| | | |   |  ||| ||||||||||||||| |
Db         73 CCTGCAAAGCTTCTGGCTACGCATTCAGTAGGTCTTGGATGAACTGGGTGAAGCAGAGGC 132

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
               |||| || | |||||||||||||||||| ||| |||||    |||| | |||    ||||
Db        133 CTGGACAGGGTCTTGAGTGGATTGGACGGATTTATCCTGGAGATGGAGATACCAAATACA 192

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |   ||| ||||||| |||||||| | | ||||  ||||  ||||||| ||||||||||
Db        193 ATGGGAAGTTCAAGGGCAAGGCCACACTGACTGCGGACAGATCATCCAGCACAGCCTACA 252

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||| |||| || |||||||||||||| |||||||| |    | |
Db        253 TGCAGCTCAGCAGCCTGACCTCTGTGGGCTCTGCGGTCTATTTCTGTGCAAAAGAGAACA 312
```

```
Qy        302 ------------TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCA 349
                          ||      |||||| |||||||||||||||| ||||  ||| | ||||
Db        313 ATAGGTTCGACGAGAGGGGTTACTATGCTATGGACTACTGGGGCCAAGGGACCACGGTCA 372

Qy        350 CCGTCTCCTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTA 409
              ||||||||||||||||| |||||     || ||||| ||  | || ||||||||||||| |
Db        373 CCGTCTCCTCAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTAACA 432

Qy        410 TTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAA 469
              ||  | |||||||| |||| |  | | ||      |||| |||||||||||| | ||| |
Db        433 TTCAGTTGACCCAGTCTCCAAATTCCATGTCCACATCAGTAGGAGACAGGGTCAGCATCA 492

Qy        470 CCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGC 529
              ||||||||||||||||  |||| || |  |||||  ||||| |||||||| ||||||||
Db        493 CCTGCAAGGCCAGTCAGGATGTGGATACTTCTGTAGCCTGGTATCAACAGAAACCAGGGC 552

Qy        530 AGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCT 589
              | ||||||| ||| || || | ||    ||||||  ||   || ||||||||||||||||
Db        553 AATCTCCTAAACTACTGATTTACTGGGCATCCACCCGGCACACTGGAGTCCCTGATCGCT 612

Qy        590 TCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAG 649
              |||  |||||||||| |||||| |||||||| |||||| |||| | |||||  ||||||
Db        613 TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAG 672

Qy        650 ACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCA 709
              ||  ||||| ||||||||||||||| ||    |  | |||   |||||||||||||| |
Db        673 ACTCGGCAGATTATTTCTGTCAGCAATATAGCAGCTATCCGTGGACGTTCGGTGGAGGGA 732

Qy        710 CCAAGCTGGAAATCAAA 726
              ||||||||| ||||||
Db        733 CCAAGCTGGAGATCAAA 749
```

RESULT 3
US-09-423-439-47
; Sequence 47, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47

Query Match 60.2%; Score 438.8; DB 3; Length 864;
Best Local Similarity 78.3%; Pred. No. 6.1e-130;
Matches 587; Conservative 0; Mismatches 137; Indels 26; Gaps 4;

```
Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || |||||| |||| |||| ||||||||||||||||||||||||| || | |
Db         68 AGGTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGCAGCTGT 127

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||||||||| ||| | ||||| |||||||  || ||||||||||||||||| |
Db        128 CCTGCAAGGCTTCTGGCTACACCTTCACCGGCTACTGGATACACTGGGTGAAGCAGAGGC 187

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| |  |||||||||||||||||     |||||||||  |  |||  | ||  |||||
Db        188 CTGGACAAGGCCTTGAGTGGATTGGAGAGGTTAATCCTAGTACCGGTCGTTCTGACTACA 247

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              | |||| |||||| |||||||||  | | ||||||||||| || ||||||||||||||||
Db        248 ATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACAAATCCTCCACCACAGCCTACA 307

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTA--- 298
              || | ||| ||||||||||||||||||||||||||||||||||||||||||||    |
Db        308 TGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGAGGG 367

Qy        299 -CTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
               ||||| |||||  || ||| |||||||||||||| |||| ||| | ||||||||||||
Db        368 CCTATGGTTACG-ACGATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCC 426

Qy        358 TCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATG 417
              |||||||| |||||      || ||||| ||  | || ||||||||||||    |||| | |
Db        427 TCAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTGACATTGAGCTC 486

Qy        418 ACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG 477
              | ||| ||||  | | ||||  ||| |||||||||| | ||| ||||| | ||||||
Db        487 TCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACCATGAGCTGCAAA 546

Qy        478 GCCAGTCAGAGTGT-----------------GAGTAATGATGTAGDTTGGTACCAACAG 519
              |||||||||||  |                 |  ||  |  | | |||||||||  |||
Db        547 TCCAGTCAGAGTCTCCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAG 606

Qy        520 AAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTC 579
              |  |||||||||||||||| |||||  || |  |    ||||||  | |      |||| |||
Db        607 AGACCAGGGCAGTCTCCTAAACTGCTGATCTATTGGGCATCCACTAGGACATCTGGGGTC 666

Qy        580 CCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTG 639
              ||||||||||||  |||||||||| |||||| |||||||| |||||||||||  | ||
Db        667 CCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTG 726

Qy        640 CAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTC 699
              |||||||||||||||||| |||||| |||  |||||  |||||    ||| || |||||||
Db        727 CAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTATA---CTCTTCGGACGTTC 783

Qy        700 GGTGGAGGCACCAAGCTGGAAATCAAACGG 729
              |||||||||||||||| || |||||||||
Db        784 GGTGGAGGCACCAAGCTCGAGATCAAACGG 813
```

RESULT 4
US-09-423-439-31
; Sequence 31, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.

```
;           ZIP: 20005
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/423,439
;           FILING DATE: 09-No. 6339070-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: PCT/GB98/01294
;           FILING DATE: 05-MAY-1998
;           APPLICATION NUMBER: GB 9709421.3
;           FILING DATE: 10-MAY-1997
;   INFORMATION FOR SEQ ID NO: 31:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 2019 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-423-439-31

  Query Match             60.2%;  Score 438.8;  DB 3;  Length 2019;
  Best Local Similarity   78.3%;  Pred. No. 9.7e-130;
  Matches  587;  Conservative    0;  Mismatches  137;  Indels   26;  Gaps    4;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || |||||| ||||  |||| ||||||||||||||||||||||| || | |
Db         59 AGGTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGCAGCTGT 118

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              ||||||||||||||| ||| | ||||| |||||||  || ||||||||||||||||| |
Db        119 CCTGCAAGGCTTCTGGCTACACCTTCACCGGCTACTGGATACACTGGGTGAAGCAGAGGC 178

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
               |||| |  |||||||||||||||||     |||||||||  |  |||  | ||  |||||
Db        179 CTGGACAAGGCCTTGAGTGGATTGGAGAGGTTAATCCTAGTACCGGTCGTTCTGACTACA 238

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |  |||| |||||| |||||||| | | |||||||||| || ||||||||||||||||
Db        239 ATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACAAATCCTCCACCACAGCCTACA 298

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTA--- 298
              || | ||| ||||||||||||||||||||||||||||||||||||||||||||    |
Db        299 TGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGAGGG 358

Qy        299 -CTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
               ||||| ||||| || ||| |||||||||||||| ||||  ||| | ||||||||||||
Db        359 CCTATGGTTACG-ACGATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCC 417

Qy        358 TCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATG 417
              |||||||| |||||    || ||||| ||  | || ||||||||||||   |||| | |
Db        418 TCAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTGACATTGAGCTC 477

Qy        418 ACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG 477
              | ||| ||||  | | |||| ||| |||||||||||| | ||| ||||| | |||||||
Db        478 TCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACCATGAGCTGCAAA 537

Qy        478 GCCAGTCAGAGTGT----------------GAGTAATGATGTAGDTTGGTACCAACAG 519
              |||||||||| |                |  ||  |  | | |||||||| |||
Db        538 TCCAGTCAGAGTCTCCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAG 597

Qy        520 AAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTC 579
              | |||||||||||||||| |||||| || |  |  |||||| | |    |||| |||
Db        598 AGACCAGGGCAGTCTCCTAAACTGCTGATCTATTGGGCATCCACTAGGACATCTGGGGTC 657

Qy        580 CCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTG 639
              |||||||||||  |||||||||| |||||| |||||||| |||||||||| | ||
Db        658 CCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTG 717

Qy        640 CAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTC 699
              ||||||||||||||||| |||||| |||  |||||  |||||   ||| || |||||||
Db        718 CAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTATA---CTCTTCGGACGTTC 774

Qy        700 GGTGGAGGCACCAAGCTGGAAATCAAACGG 729
              |||||||||||||||| || |||||||||
Db        775 GGTGGAGGCACCAAGCTCGAGATCAAACGG 804


RESULT 5
US-09-423-439-37
; Sequence 37, Application US/09423439
; Patent No. 6339070
;   GENERAL INFORMATION:
;       APPLICANT: EMERY, Stephen Charles
;                  BLAKEY, David Charles
;       TITLE OF INVENTION: CHEMICAL COMPOUNDS
;       NUMBER OF SEQUENCES: 60
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Pillsbury Winthrop, L.L.P.
;           STREET: 1100 New York Ave., N.W.
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: U.S.A.
;           ZIP: 20005
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/423,439
;           FILING DATE: 09-No. 6339070-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: PCT/GB98/01294
;           FILING DATE: 05-MAY-1998
;           APPLICATION NUMBER: GB 9709421.3
;           FILING DATE: 10-MAY-1997
;   INFORMATION FOR SEQ ID NO: 37:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 2025 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-423-439-37

  Query Match             60.2%;  Score 438.8;  DB 3;  Length 2025;
  Best Local Similarity   78.3%;  Pred. No. 9.7e-130;
  Matches  587;  Conservative    0;  Mismatches  137;  Indels   26;  Gaps    4;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || |||||| ||||  |||| ||||||||||||||||||||||| || | |
Db         59 AGGTCCAACTGCAGCAGCCTGGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGCAGCTGT 118

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              ||||||||||||||| ||| | ||||| |||||||  || ||||||||||||||||| |
Db        119 CCTGCAAGGCTTCTGGCTACACCTTCACCGGCTACTGGATACACTGGGTGAAGCAGAGGC 178

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
               |||| |  |||||||||||||||||     |||||||||  |  |||  | ||  |||||
Db        179 CTGGACAAGGCCTTGAGTGGATTGGAGAGGTTAATCCTAGTACCGGTCGTTCTGACTACA 238

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |  |||| |||||| |||||||| | | |||||||||| || ||||||||||||||||
Db        239 ATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACAAATCCTCCACCACAGCCTACA 298

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTA--- 298
              || | ||| ||||||||||||||||||||||||||||||||||||||||||||    |
Db        299 TGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGAGGG 358
```

```
Qy        299 -CTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
              ||||| ||||| || ||| ||||||||||||||| ||||  ||| | ||||||||||||
Db        359 CCTATGGTTACG-ACGATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCC 417

Qy        358 TCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATG 417
              |||||||| |||||     || ||||| ||  | || ||||||||||||    |||| | |
Db        418 TCAGGTGGCGGTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGCGGATCTGACATTGAGCTC 477

Qy        418 ACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG 477
              | ||| ||||  | | ||||  ||| |||||||||||| | ||| |||||  | ||||||
Db        478 TCACAGTCTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGAAGGTCACCATGAGCTGCAAA 537

Qy        478 GCCAGTCAGAGTGT------------------GAGTAATGATGTAGDTTGGTACCAACAG 519
              |||||||||||  |                  ||  |  | | |||||||||  |||
Db        538 TCCAGTCAGAGTCTCCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGGTACCAGCAG 597

Qy        520 AAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTC 579
              |  |||||||||||||||| |||||| || |  |   |||||| | |      |||| |||
Db        598 AGACCAGGGCAGTCTCCTAAACTGCTGATCTATTGGGCATCCACTAGGACATCTGGGGTC 657

Qy        580 CCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTG 639
              ||||||||||||  |||||||||| |||||| |||||||| ||||||||||| | ||
Db        658 CCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTG 717

Qy        640 CAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTC 699
              |||||||||||||||||| |||||| |||  |||||  |||||   ||| || |||||||
Db        718 CAGGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTATA---CTCTTCGGACGTTC 774

Qy        700 GGTGGAGGCACCAAGCTGGAAATCAAACGG 729
              |||||||||||||||| || |||||||||
Db        775 GGTGGAGGCACCAAGCTCGAGATCAAACGG 804
```

RESULT 6
US-10-092-246-5
; Sequence 5, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-5

Query Match 57.8%; Score 421.6; DB 4; Length 777;
Best Local Similarity 75.0%; Pred. No. 1.9e-124;
Matches 546; Conservative 1; Mismatches 166; Indels 15; Gaps 1;

```
Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| ||||||||||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 67

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |  | ||||||||||  || |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||   | | |||||      | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
                  |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||||||||||||| | || |||||||  |||||||||   |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                          |   | |||||||||| |||| ||| | ||||||||||||||||
Db        304 ----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||    || || || ||| ||||||| ||||||||    || | | | || |
Db        353 GTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||||| |||| | |     ||| |||||||||| | |  || ||||||||||||||
Db        413 AGTCTCCCAAATTCGTTGTCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| ||||||| ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   |||||| ||  || ||||||||||||||||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGATCGCTTCACAGGCAGTG 592

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| |||||| |||||||| |||||| |||| |  |||| |||||||| |||||| ||
Db        593 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGCGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||||| ||| ||   | | |||   |||||||    || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720
```

RESULT 7
US-10-096-246A-5
; Sequence 5, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 777
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(777)
; OTHER INFORMATION: scFv protein MA116-14 1 - 720
; OTHER INFORMATION: e-tag 721 - 777
US-10-096-246A-5

Query Match 57.8%; Score 421.6; DB 4; Length 777;
Best Local Similarity 75.0%; Pred. No. 1.9e-124;
Matches 546; Conservative 1; Mismatches 166; Indels 15; Gaps 1;

```
Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| ||||||||||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 67
```

```
Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |  | ||||||||||||  ||  |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||   | | |||||      | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||||||||||||| | || |||||||  |||||||||  |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                          |   | ||||||||||| ||||  ||| | ||||||||||||||||
Db        304 -----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||    || || || ||| |||||||| ||||||||    || | | | || |
Db        353 GTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||||| |||| |  |    |||  |||||||||| | |  || ||||||||||||
Db        413 AGTCTCCCAAATTCGTTGTCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| ||||||| ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   ||||||  ||  || ||||||||||||||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGATCGCTTCACAGGCAGTG 592

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| |||||| |||||||| |||||||| |||| |  |||| |||||||| |||||| ||
Db        593 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGCGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||||| ||| ||   |  | |||   |||||||   || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720


RESULT 8
US-10-092-246-7
; Sequence 7, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-7

  Query Match             57.2%;  Score 416.8;  DB 4;  Length 777;
  Best Local Similarity   74.6%;  Pred. No. 6.4e-123;
  Matches  543;  Conservative    1;  Mismatches  169;  Indels   15;  Gaps    1;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| |||||||||||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 67

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |  | ||||||||||||  ||  |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||   | | |||||      | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||||||||||||| | || |||||||  |||||||||  |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                          |   | ||||||||||| ||||  ||| | ||||||||||||||||
Db        304 -----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||    || || || ||| |||||||| ||||||||    || | | | || |
Db        353 GTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| |  |   ||      |||  |||||||||| | |  || ||||||||||||
Db        413 AGTCTCCAAATTCGTTGTCCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| ||||||| ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   ||||||  ||  || ||||||||||||||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGATCGCTTCACAGGCAGTG 592

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| |||||| |||||||| |||||||| |||| |  |||| |||||||| |||||| ||
Db        593 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||||| ||| ||   |  | |||   |||||||   || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720


RESULT 9
US-10-096-246A-7
; Sequence 7, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
```

```
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: mouse
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(777)
;   OTHER INFORMATION: scFv protein MA116-15  1 - 720
;   OTHER INFORMATION: e-tag          721 - 777
US-10-096-246A-7

  Query Match             57.2%;  Score 416.8;  DB 4;  Length 777;
  Best Local Similarity   74.6%;  Pred. No. 6.4e-123;
  Matches  543;  Conservative    1;  Mismatches  169;  Indels   15;  Gaps    1;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| ||||||||||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 67

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |  | ||||||||||||  ||  |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||    | | |||||       | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| ||||||||||||||||||||| | || |||||||  |||||||||  |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                          |   | |||||||||||| ||||  ||| | ||||||||||||||||
Db        304 -----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||    || || || ||| |||||| ||||||||    || | | | || |
Db        353 GTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| | |   ||      ||| |||||||||| | |  || ||||||||||||||
Db        413 AGTCTCCAAATTCGTTGTCCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| |||||||  ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   |||||| ||  || ||||||||||||||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGATCGCTTCACAGGCAGTG 592

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| |||||| |||||||| ||||||| |||| | ||||| |||||||| |||||| ||
Db        593 GATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||||| ||| ||    |  | |||     ||||||||     || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720


RESULT 10
US-09-581-345-1
; Sequence 1, Application US/09581345
; Patent No. 6809184
; GENERAL INFORMATION:
;  APPLICANT: Pastan, Ira H.
;  APPLICANT: Chowdhury, Partha S.
;  APPLICANT: The Government of the United States
;  APPLICANT: as represented by The Secretary of the
;  APPLICANT: Department of Health and Human Services
;  TITLE OF INVENTION: Antibodies, Including Fv Molecules, and
;  TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
;  TITLE OF INVENTION: Mesothelin and Methods for Their Use
;  FILE REFERENCE: 015280-339100US
;  CURRENT APPLICATION NUMBER: US/09/581,345
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER: US 60/067,175
;  PRIOR FILING DATE: 1997-12-01
;  PRIOR APPLICATION NUMBER: WO PCT/US98/25270
;  PRIOR FILING DATE: 1998-11-25
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SS scFv
US-09-581-345-1

  Query Match             56.8%;  Score 413.8;  DB 4;  Length 723;
  Best Local Similarity   75.0%;  Pred. No. 5.6e-122;
  Matches  544;  Conservative    1;  Mismatches  174;  Indels    6;  Gaps    2;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              |||| || || |||||||||| ||||| |||| |||||||| ||||||||||||||||||
Db          5 AGGTACAACTGCAGCAGTCTGGGCCTGAGCTGGAGAAGCCTGGCGCTTCAGTGAAGATAT 64

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||||||||||||||||||||||||||||||||  |||| ||||||||||||||||
Db         65 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACACCATGAACTGGGTGAAGCAGAGCC 124

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||||||||||||||||||||||||||| ||||| |||| |||||||| | ||  |||||
Db        125 ATGGAAAGAGCCTTGAGTGGATTGGACTTATTACTCCTTACAATGGTGCTTCTAGCTACA 184

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              ||||||| |||| || |||||||| |||||||||||||||||||||||| ||||||||||
Db        185 ACCAGAAGTTCAGGGGCAAGGCCACATTAACTGTAGACAAGTCATCCAGCACAGCCTACA 244

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              |||| |||| ||| |||||||||| ||||||| ||||||| ||||||||        |
Db        245 TGGACCTCCTCAGTCTGACATCTGAAGACTCTGCAGTCTATTTCTGTGCAAGGGGGGGTT 304

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                        ||    | | | |||||||||| ||||   ||| | ||||||||||||||||
Db        305 ACGACGGGA---GGGGTTTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 361

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||  || ||     || || || ||| ||||||| ||||||||    || | | | || |
Db        362 GTGTAGGCGGTTCAGGCGGCGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 421

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| || || ||  ||  || |||| || | ||| |||| |||||||  ||||
Db        422 AGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCA 481

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |    ||||| ||   | |  |  : |||||||| |||||| ||||    || || | |
Db        482 GCTCAAGTGTAAG---TTACATGCACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAA 538

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              || |   | |||||||  |        |||||||||| | |||||||| ||||||||
Db        539 GATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTTCAGTGGCAGTG 598

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              | | ||| |    || | || |||| |||||||    || ||||||||||    |||  ||
Db        599 GGTCTGGAAACTCTTACTCTCTCACAATCAGCAGCGTGGAGGCTGAAGATGATGCAACTT 658

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
```

```
Db        659 ATTACTGCCAGCAGTGGAGTGGTTACCCTCTCACGTTCGGTGCTGGGACAAAGTTGGAAA 718

Qy        722 TCAAA 726
              | |||
Db        719 TAAAA 723
```

RESULT 11
US-10-092-246-6
; Sequence 6, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-6

Query Match 56.5%; Score 412; DB 4; Length 777;
Best Local Similarity 74.2%; Pred. No. 2.2e-121;
Matches 540; Conservative 1; Mismatches 172; Indels 15; Gaps 1;

```
Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| ||||||||| ||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGTCTGGGGCTTCAGTGAAGATAT 67

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |   | ||||||||||||  ||  |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||    | | |||||       | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||||||||||||| | || |||||||  |||||||||  |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                    |  | |||||||||||| ||||  ||| | ||||||||||||||||
Db        304 ----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||   || || || ||| ||||||| ||||||||    || | | | || |
Db        353 GTGGGGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| |  |   ||      |||  |||||||||| | |  || ||||||||||||
Db        413 AGTCTCCAAATTCGTTGTCCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| ||||||| ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   |||||  ||  || |||||||||||||| |||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGACCGCTTCACAGGCAGTG 592

```
Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| ||| || ||||||||| ||||||| |||| | ||||| |||||||| |||||| ||
Db        593 GATCTGGAACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              |||||||||| ||| ||   |  | |||    ||||||||    || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720
```

RESULT 12
US-10-096-246A-6
; Sequence 6, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 777
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(777)
; OTHER INFORMATION: scFv protein MA116-16 1 - 720
; OTHER INFORMATION: e-tag 721 - 777
US-10-096-246A-6

Query Match 56.5%; Score 412; DB 4; Length 777;
Best Local Similarity 74.2%; Pred. No. 2.2e-121;
Matches 540; Conservative 1; Mismatches 172; Indels 15; Gaps 1;

```
Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||||| || ||| |||| |||||||| ||||||||| ||||||||||||||||||||||
Db          8 AGGTCCAACTGCAGGAGTCAGGACCTGAGCTGGTGAAGTCTGGGGCTTCAGTGAAGATAT 67

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||||| ||||| ||| | ||||||| |||| |   | ||||||||||||  ||  |
Db         68 CCTGCAAGGCCTCTGGCTACACCTTCACTGACTACCATGTTCACTGGGTGAAGGGGAAGC 127

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||| || | ||||| |||||||||    | | |||||       | |  ||||   ||||
Db        128 CTGGACAGGGACTTGAATGGATTGGAATGACTTATCCTGGATTCGATAATACTAATTACA 187

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              |||  ||||||| |||||||| ||| ||||||||||  || |||| ||||| |||||
Db        188 GTGAGACTTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCTCCAACACAGTCTACA 247

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              || ||||| |||||||||||||||||||| | || |||||||  |||||||||  |
Db        248 TGCAGCTCAGCAGCCTGACATCTGAGGACACCGCTGTCTATTTTTGTGCAAGAGGT---- 303

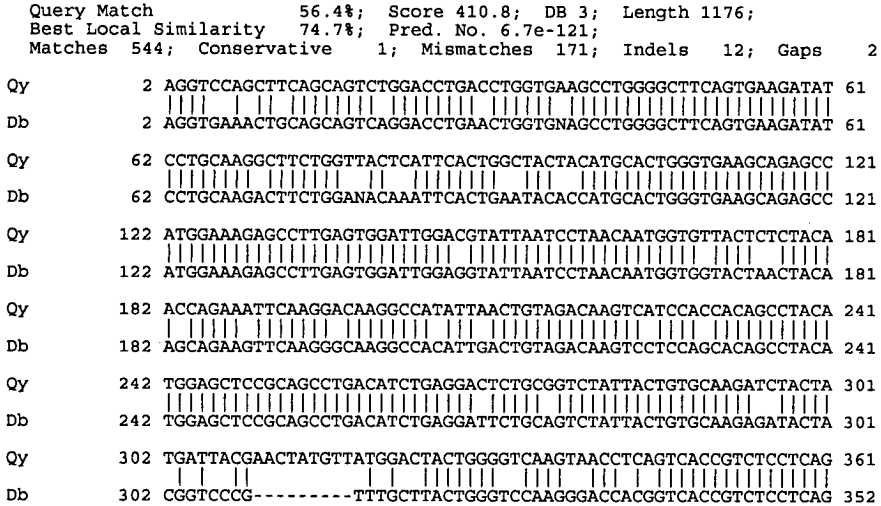
Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                    |  | |||||||||||| ||||  ||| | ||||||||||||||||
Db        304 ----------GTGGGCCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||   || || || ||| ||||||| ||||||||    || | | | || |
Db        353 GTGGGGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412
```
```

```
Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| |  |   ||  .  |||  |||||||||| | |  || ||||||||||||||
Db        413 AGTCTCCAAATTCGTTGTCCACATCAATAGGAGACAGGATCAGAATCACCTGCAAGGCCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |||||  ||||  || || |||||: ||||| |||||||  |||||||| ||||||| ||
Db        473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              | || || | ||   ||||||  ||  || ||||||||||||| |||||||  |||||||
Db        533 TACTGATTTTCTGGTCATCCACCCGGCACACTGGAGTCCCTGACCGCTTCACAGGCAGTG 592

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              ||| ||| || ||||||||| ||||||| |||| | ||||| ||||||||  |||||| ||
Db        593 GATCTGGAACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATT 652

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              ||||||||||  ||| ||   |  | |||    ||||||||    || || ||| ||||||
Db        653 ATTTCTGTCACCAATATAGCAGCTATCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAA 712

Qy        722 TCAAACGG 729
              | ||||||
Db        713 TAAAACGG 720


RESULT 13
US-09-142-974B-1
; Sequence 1, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
;  APPLICANT:  Cheung, Nai-Kong V.
;  APPLICANT:  Larson, Steven M.
;  APPLICANT:  Guo, Hong-Fen
;  APPLICANT:  Rivlin, Ken
;  APPLICANT:  Sadelain, Michel
;  TITLE OF INVENTION:  Single Chain FV Constructs of Anti-Ganglioside GD2
;  TITLE OF INVENTION:  Antibodies
;  FILE REFERENCE:  MSK.P-013-USNP
;  CURRENT APPLICATION NUMBER: US/09/142,974B
;  CURRENT FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PCT/US97/04427
;  PRIOR FILING DATE:  1997-03-20
;  PRIOR APPLICATION NUMBER:  60/013,703
;  PRIOR FILING DATE:  1996-03-20
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Murine
;   FEATURE:
;   OTHER INFORMATION: 5F11-scFv
;   NAME/KEY: unsure
;   LOCATION: (37)
;   NAME/KEY: unsure
;   LOCATION: (79)
US-09-142-974B-1

  Query Match             56.4%;  Score 410.8;  DB 3;  Length 717;
  Best Local Similarity   74.7%;  Pred. No. 5.1e-121;
  Matches  544;  Conservative    1;  Mismatches  171;  Indels   12;  Gaps    2;

Qy          2 AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT 61
              ||||  | || |||||||| |||||||| |||||| ||||||||||||||||||||||||
Db          2 AGGTGAAACTGCAGCAGTCAGGACCTGAACTGGTGNAGCCTGGGGCTTCAGTGAAGATAT 61

Qy         62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121
              |||||||| |||||||  ||  ||||||||  |||  ||||||||||||||||||||||
Db         62 CCTGCAAGACTTCTGGANACAAATTCACTGAATACACCATGCACTGGGTGAAGCAGAGCC 121

Qy        122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACA 181
              |||||||||||||||||||||||||| |||||||||||||||||||| ||||  |||||
Db        122 ATGGAAAGAGCCTTGAGTGGATTGGAGGTATTAATCCTAACAATGGTGGTACTAACTACA 181

Qy        182 ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACA 241
              | ||||| ||||||| |||||||| ||| |||||||||||||| |||| ||||||||||
Db        182 AGCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTACA 241

Qy        242 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301
              ||||||||||||||||||||||||||||||| ||||| ||||||||||||||||  |||||
Db        242 TGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACTA 301

Qy        302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
              | |  ||          | |  |||||||  ||||  ||| | ||||||||||||||||
Db        302 CGGTCCCG---------TTTGCTTACTGGGTCCAAGGGACCACGGTCACCGTCTCCTCAG 352

Qy        362 GTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCC 421
              |||| || ||    || || || ||| ||||||| ||||||||    || | | | || |
Db        353 GTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATCGAGCTCACTC 412

Qy        422 AGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCA 481
              || |||| || || ||  ||  ||  |||| || | ||| ||||  ||||||| | ||
Db        413 AGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGGCA 472

Qy        482 GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC 541
              |   ||| | ||   | |  |  : |||||||| |||||||| |     || || | |
Db        473 GCTCAAGTATAAG---TTACATGCACTGGTACCAGCAGAAGCCTGTCACCTCCCCCAAAA 529

Qy        542 TGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG 601
              || |   | |||||||  |       |||||||||||| |||||||| ||||||||
Db        530 GATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTG 589

Qy        602 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT 661
              | | ||||||   ||   || |||| |||||||   || |||||| |||    ||   ||
Db        590 GGTCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGTAGATGCTGCCACTT 649

Qy        662 ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA 721
              ||| ||| || ||       || ||  || |  |||||||||  || ||  || ||||||
Db        650 ATTACTGCCATCAGCGGAGTAGTTACCCGCTCACGTTCGGTGCTGGGACACAGTTGGAAA 709

Qy        722 TCAAACGG 729
              | ||||||
Db        710 TAAAACGG 717


RESULT 14
US-09-142-974B-3
; Sequence 3, Application US/09142974B
; Patent No. 6451995
; GENERAL INFORMATION:
;  APPLICANT:  Cheung, Nai-Kong V.
;  APPLICANT:  Larson, Steven M.
;  APPLICANT:  Guo, Hong-Fen
;  APPLICANT:  Rivlin, Ken
;  APPLICANT:  Sadelain, Michel
;  TITLE OF INVENTION:  Single Chain FV Constructs of Anti-Ganglioside GD2
;  TITLE OF INVENTION:  Antibodies
;  FILE REFERENCE:  MSK.P-013-USNP
;  CURRENT APPLICATION NUMBER: US/09/142,974B
;  CURRENT FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PCT/US97/04427
;  PRIOR FILING DATE:  1997-03-20
;  PRIOR APPLICATION NUMBER:  60/013,703
;  PRIOR FILING DATE:  1996-03-20
;  NUMBER OF SEQ ID NOS:  5
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1176
;   TYPE: DNA
;   ORGANISM: Murine
;   FEATURE:
;   OTHER INFORMATION: 5F11-scFv-streptavidin
;   NAME/KEY: unsure
;   LOCATION: (37)
;   NAME/KEY: unsure
;   LOCATION: (79)
```

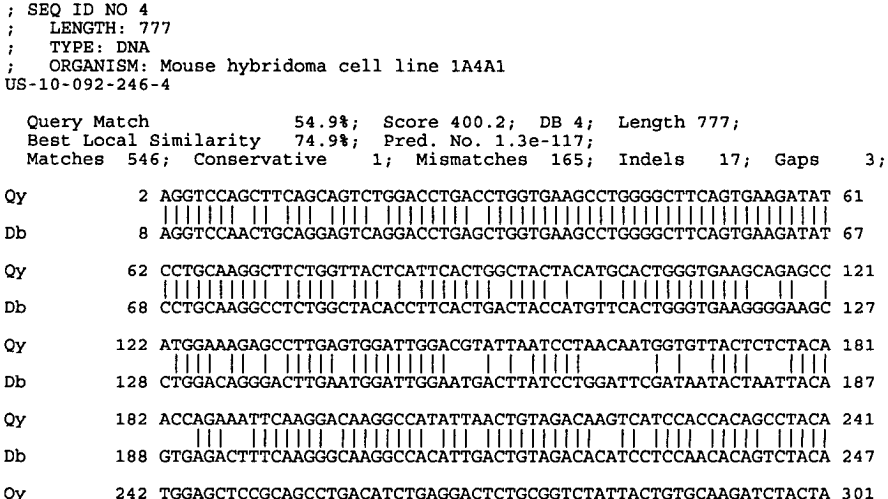
US-09-142-974B-3

Query Match 56.4%; Score 410.8; DB 3; Length 1176;
Best Local Similarity 74.7%; Pred. No. 6.7e-121;
Matches 544; Conservative 1; Mismatches 171; Indels 12; Gaps 2;



RESULT 15
US-10-092-246-4
; Sequence 4, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-4

Query Match 54.9%; Score 400.2; DB 4; Length 777;
Best Local Similarity 74.9%; Pred. No. 1.3e-117;
Matches 546; Conservative 1; Mismatches 165; Indels 17; Gaps 3;



Search completed: March 14, 2005, 22:55:25
Job time : 194 secs

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 20:12:30 ; Search time 574 Seconds
(without alignments)
7554.836 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	728.2	99.9	729	14	US-10-060-585-1	Sequence 1, Appli
2	728.2	99.9	729	18	US-10-334-235-1	Sequence 1, Appli
3	728.2	99.9	729	19	US-10-787-881A-1	Sequence 1, Appli
4	727.4	99.8	1807	14	US-10-060-585-2	Sequence 2, Appli
5	727.4	99.8	1807	18	US-10-334-235-2	Sequence 2, Appli
6	727.4	99.8	1807	19	US-10-787-881A-2	Sequence 2, Appli
7	724.4	99.4	1467	14	US-10-060-585-3	Sequence 3, Appli
8	724.4	99.4	1467	18	US-10-334-235-3	Sequence 3, Appli
9	724.4	99.4	1467	19	US-10-787-881A-3	Sequence 3, Appli
10	724.2	99.3	1518	14	US-10-104-522-5	Sequence 5, Appli
11	724.2	99.3	1518	14	US-10-060-585-5	Sequence 5, Appli
12	724.2	99.3	1518	18	US-10-334-235-5	Sequence 5, Appli
13	724.2	99.3	1518	19	US-10-787-881A-5	Sequence 5, Appli
14	722.6	99.1	9100	18	US-10-334-235-16	Sequence 16, Appl
15	721	98.9	2090	14	US-10-104-522-6	Sequence 6, Appli
16	721	98.9	2090	14	US-10-060-585-6	Sequence 6, Appli
17	721	98.9	2090	18	US-10-334-235-6	Sequence 6, Appli
18	721	98.9	2090	19	US-10-787-881A-6	Sequence 6, Appli
19	505.4	69.3	729	19	US-10-879-994-9	Sequence 9, Appli
20	481.2	66.0	10511	14	US-10-059-261-109	Sequence 109, App
21	481.2	66.0	10511	18	US-10-627-649-109	Sequence 109, App
22	458.2	62.9	756	9	US-09-984-186-17	Sequence 17, Appl
23	458.2	62.9	756	14	US-10-237-667-17	Sequence 17, Appl
24	458.2	62.9	756	14	US-10-237-708-17	Sequence 17, Appl
25	458.2	62.9	756	14	US-10-237-866-17	Sequence 17, Appl
26	458.2	62.9	756	14	US-10-237-871-17	Sequence 17, Appl
27	458.2	62.9	756	14	US-10-237-624-17	Sequence 17, Appl
28	458.2	62.9	756	17	US-10-702-536-17	Sequence 17, Appl
29	458.2	62.9	756	17	US-10-702-636-17	Sequence 17, Appl
30	439.4	60.3	759	9	US-09-978-752-10	Sequence 10, Appl
31	432.8	59.4	795	14	US-10-114-716A-47	Sequence 47, Appl
32	430.8	59.1	2952	18	US-10-296-085A-30	Sequence 30, Appl
33	424.4	58.2	723	18	US-10-405-123-2	Sequence 2, Appli
34	421.6	57.8	777	15	US-10-096-246-5	Sequence 5, Appli
35	418.4	57.4	774	17	US-10-239-656-58	Sequence 58, Appl
36	417.2	57.2	720	18	US-10-482-630-52	Sequence 52, Appl
37	417.2	57.2	726	15	US-10-259-087A-19	Sequence 19, Appl
38	417.2	57.2	726	18	US-10-689-006-19	Sequence 19, Appl
39	416.8	57.2	777	15	US-10-096-246-7	Sequence 7, Appli
40	416.8	57.2	1869	17	US-10-378-832A-1	Sequence 1, Appli
41	414.2	56.8	910	14	US-10-104-522-1	Sequence 1, Appli
42	413	56.7	1920	17	US-10-120-198B-1	Sequence 1, Appli
43	413	56.7	6834	17	US-10-120-198B-5	Sequence 5, Appli
44	412	56.5	777	15	US-10-096-246-6	Sequence 6, Appli
45	410.8	56.4	717	8	US-08-940-544-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYOU23.001CP1
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```
;   OTHER INFORMATION: 5T4 ScFv
US-10-060-585-1

  Query Match             99.9%;  Score 728.2;  DB 14;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-224;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 2
US-10-334-235-1
; Sequence 1, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding a 5T4 scFv, designated 5T4scFv.1
US-10-334-235-1

  Query Match             99.9%;  Score 728.2;  DB 18;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-224;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
```

```
                 |||||||||
Db        721 ATCAAACGG 729


RESULT 3
US-10-787-881A-1
; Sequence 1, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
;  APPLICANT: Oxford BioMedica (UK) Ltd.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: Vector
;  FILE REFERENCE: 021911-000330US
;  CURRENT APPLICATION NUMBER: US/10/787,881A
;  CURRENT FILING DATE:  2004-02-25
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/01627
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Coding sequence of 5T4scFv
US-10-787-881A-1

  Query Match             99.9%;  Score 728.2;  DB 19;  Length 729;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-224;
  Matches  729;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720

Qy        721 ATCAAACGG 729
              |||||||||
Db        721 ATCAAACGG 729


RESULT 4
US-10-060-585-2
; Sequence 2, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
;  APPLICANT: Kingsman, Alan J.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 5T4Sab1
US-10-060-585-2

  Query Match             99.8%;  Score 727.4;  DB 14;  Length 1807;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-224;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308
```

```
Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 5
US-10-334-235-2
; Sequence 2, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxfard Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA sequence encoding 5T4Sab1
US-10-334-235-2

Query Match 99.8%; Score 727.4; DB 18; Length 1807;
Best Local Similarity 99.9%; Pred. No. 2.9e-224;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797
```

RESULT 6
US-10-787-881A-2
; Sequence 2, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
; APPLICANT: Oxford BioMedica (UK) Ltd.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: Vector
; FILE REFERENCE: 021911-000330US
; CURRENT APPLICATION NUMBER: US/10/787,881A
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627

```
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1807
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence encoding 5T4 single chain antibody
US-10-787-881A-2

  Query Match            99.8%;  Score 727.4;  DB 19;  Length 1807;
  Best Local Similarity  99.9%;  Pred. No. 2.9e-224;
  Matches  728;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
Db        789 ATCAAACGG 797


RESULT 7
US-10-060-585-3
; Sequence 3, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
;  APPLICANT: Kingsman, Alan J.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7-1.5T4.1
US-10-060-585-3

  Query Match            99.4%;  Score 724.4;  DB 14;  Length 1467;
  Best Local Similarity  99.9%;  Pred. No. 2.5e-223;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
                 ||||||
Db       1459 ATCAAA 1464


RESULT 8
US-10-334-235-3
; Sequence 3, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence of B7-1.5T4.1
US-10-334-235-3

  Query Match             99.4%;  Score 724.4;  DB 18;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 2.5e-223;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                 |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
                 ||||||
Db       1459 ATCAAA 1464


RESULT 9
US-10-787-881A-3
; Sequence 3, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
;  APPLICANT: Oxford BioMedica (UK) Ltd.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: Vector
;  FILE REFERENCE: 021911-000330US
;  CURRENT APPLICATION NUMBER: US/10/787,881A
;  CURRENT FILING DATE:  2004-02-25
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/01627
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence encoding fusion protein B7-1.5T4.1
US-10-787-881A-3

  Query Match             99.4%;  Score 724.4;  DB 19;  Length 1467;
  Best Local Similarity   99.9%;  Pred. No. 2.5e-223;
  Matches  725;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 798

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 858
```

```
Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1038

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 1098

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1158

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1218

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1338

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1399 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458

Qy        721 ATCAAA 726
              ||||||
Db       1459 ATCAAA 1464
```

RESULT 10
US-10-104-522-5
; Sequence 5, Application US/10104522
; Publication No. US20030018004A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, C.R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: DYOU23.001DV1
; CURRENT APPLICATION NUMBER: US/10/104,522
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/445375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBSII/Leader/scFv/HG1.
US-10-104-522-5

Query Match 99.3%; Score 724.2; DB 14; Length 1518;
Best Local Similarity 99.6%; Pred. No. 2.9e-223;
Matches 726; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515
```

RESULT 11
US-10-060-585-5
; Sequence 5, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.

```
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: DYOU23.001CP1
;  CURRENT APPLICATION NUMBER: US/10/060,585
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/445375
;  PRIOR FILING DATE: 1998-06-04
;  PRIOR APPLICATION NUMBER: GB 9711579.4
;  PRIOR FILING DATE: 1997-06-04
;  PRIOR APPLICATION NUMBER: GB 9713150.2
;  PRIOR FILING DATE: 1997-06-20
;  PRIOR APPLICATION NUMBER: GB 9714230.1
;  PRIOR FILING DATE: 1997-07-04
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB99/03859
;  PRIOR FILING DATE: 1999-11-18
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7 link ScFv sequence
US-10-060-585-5

  Query Match             99.3%;  Score 724.2;  DB 14;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-223;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
              |||||||||
Db       1507 ATCAAACGG 1515


RESULT 12
US-10-334-235-5
; Sequence 5, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: B7 Link scFv sequence
US-10-334-235-5

  Query Match             99.3%;  Score 724.2;  DB 18;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-223;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                 |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
                 |||||||||
Db       1507 ATCAAACGG 1515


RESULT 13
US-10-787-881A-5
; Sequence 5, Application US/10787881A
; Publication No. US20050032216A1
; GENERAL INFORMATION:
;  APPLICANT: Oxford BioMedica (UK) Ltd.
;  APPLICANT:  Kingsman, Susan M.
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Ellard, Fiona M.
;  APPLICANT:  Carroll, Miles W.
;  APPLICANT:  Myers, Kevin A.
;  TITLE OF INVENTION: Vector
;  FILE REFERENCE: 021911-000330US
;  CURRENT APPLICATION NUMBER: US/10/787,881A
;  CURRENT FILING DATE:  2004-02-25
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/01627
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence encoding B7 Link scFv
US-10-787-881A-5

  Query Match             99.3%;  Score 724.2;  DB 19;  Length 1518;
  Best Local Similarity   99.6%;  Pred. No. 2.9e-223;
  Matches  726;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 846

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 906

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 966

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 1026

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 1086

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                 |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       1087 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 1146

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 1206

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
                 |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 1386

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1446

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506

Qy        721 ATCAAACGG 729
                 |||||||||
Db       1507 ATCAAACGG 1515


RESULT 14
US-10-334-235-16
; Sequence 16, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
;  APPLICANT: Oxfard Biomedica (UK) Ltd.
;  APPLICANT:  Kingsman, Alan
;  APPLICANT:  Bebbington, Christopher
;  APPLICANT:  Carroll, Miles
;  APPLICANT:  Ellard, Fiona
;  APPLICANT:  Kingsman, Susan
;  APPLICANT:  Myers, Kevin
;  APPLICANT:  Lamikandra, Abigail
;  TITLE OF INVENTION: VECTOR SYSTEM
;  FILE REFERENCE: 532682000920
;  CURRENT APPLICATION NUMBER: US/10/334,235
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 10/060,585
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/GB00/04317
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: US 09/445,375
;  PRIOR FILING DATE: 1998-06-04
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 9100
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: nuc sequence of the SMART2 LscFvB7.1 5' cPPT
;   OTHER INFORMATION: plasmid
```

US-10-334-235-16

Query Match 99.1%; Score 722.6; DB 18; Length 9100;
Best Local Similarity 99.5%; Pred. No. 2.1e-222;
Matches 725; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 3706

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 3766

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 3826

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 3886

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 3946

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db       3947 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 4006

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4007 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 4066

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4067 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 4126

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       4127 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 4186

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4187 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 4246

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4247 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 4306

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4307 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 4366

Qy        721 ATCAAACGG 729
              || |||||||
Db       4367 ATAAAACGG 4375
```

RESULT 15
US-10-104-522-6
; Sequence 6, Application US/10104522
; Publication No. US20030018004A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Bebbington, C.R.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Carroll, Miles W.
; TITLE OF INVENTION: VECTOR
; FILE REFERENCE: DYOU23.001DV1
; CURRENT APPLICATION NUMBER: US/10/104,522
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/445375
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/GB98/01627
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB9714230.1
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5T4 scFv-human IgE fusion construct.
US-10-104-522-6

Query Match 98.9%; Score 721; DB 14; Length 2090;
Best Local Similarity 99.3%; Pred. No. 3.6e-222;
Matches 724; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
              |||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
Db        369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428

Qy        361 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488

Qy        421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 548

Qy        481 AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 608

Qy        541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 668

Qy        601 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728

Qy        661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788

Qy        721 ATCAAACGG 729
              |||||||||
```

Db 789 ATCAAACGG 797

Search completed: March 15, 2005, 00:12:29
Job time : 577 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 18:20:07 ; Search time 3220 Seconds
(without alignments)
8617.656 Million cell updates/sec

Title: US-10-016-686-5
Perfect score: 729
Sequence: 1 gaggtccagcttcagcagtc.....ccaagctggaaatcaaacgg 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	291	39.9	872	7	CK629396	CK629396 AM0-AA001
c 2	284.4	39.0	601	5	BQ474958	BQ474958 carabus4g
c 3	283.4	38.9	1104	7	CK629846	CK629846 AM2-AA002
4	282.4	38.7	1010	5	BQ921928	BQ921928 AGENCOURT
5	280.8	38.5	594	2	BE309592	BE309592 601094848
6	273.8	37.6	724	2	BF168514	BF168514 601775412
7	272.2	37.3	769	2	BF168856	BF168856 601775314
8	270	37.0	507	2	BF015548	BF015548 uy23a08.y
c 9	269.4	37.0	1419	7	CK629415	CK629415 AM1-AA001
10	268	36.8	883	2	BF580610	BF580610 602093730
11	266.6	36.6	931	5	BU523606	BU523606 AGENCOURT
c 12	264.4	36.3	1339	7	CK629414	CK629414 AM1-AA001
13	263.6	36.2	598	4	BI104341	BI104341 602889919
14	262	35.9	842	9	BX969451	BX969451 Reverse s
15	261	35.8	684	2	BF577847	BF577847 602092155
16	260.6	35.7	610	7	CF912857	CF912857 A0638H09-
17	260.2	35.7	1039	5	BQ959855	BQ959855 AGENCOURT
18	260	35.7	672	7	CK633068	CK633068 AM3-AP001
19	260	35.7	672	7	CK633069	CK633069 AM3-AP001
20	259.6	35.6	640	5	BQ109114	BQ109114 imageqc_6
21	259.2	35.6	899	4	BG973020	BG973020 602838676
22	251.6	34.5	506	6	CA578474	CA578474 K0724C11-
23	251.6	34.5	506	6	CA578686	CA578686 K0727C05-
24	251.6	34.5	823	7	CK632348	CK632348 AM0-AM000
25	251	34.4	616	2	BF136295	BF136295 601781413
26	251	34.4	941	2	BF138189	BF138189 601781314
27	250.4	34.3	934	2	BF139595	BF139595 601785525
28	249.6	34.2	933	5	BQ929209	BQ929209 AGENCOURT
29	249.2	34.2	685	2	BF136104	BF136104 601783550
30	249	34.2	783	2	BF143757	BF143757 601789643
31	246	33.7	784	8	BH121432	BH121432 RPCI-24-3
32	244	33.5	670	2	BF141092	BF141092 601786180
33	243.6	33.4	690	4	BG968682	BG968682 602836513
34	243.6	33.4	819	4	BG966397	BG966397 602832896
35	243.2	33.4	811	4	BG966605	BG966605 602834440
36	243	33.3	565	2	BF801321	BF801321 MR0-CI002
37	242	33.2	465	6	CA578116	CA578116 K0718G11-
38	242	33.2	732	4	BI456459	BI456459 603171884
39	241.8	33.2	473	6	CA580167	CA580167 K0747G08-
40	241.8	33.2	519	6	CA580087	CA580087 K0746G01-
41	241.8	33.2	540	6	CA579750	CA579750 K0741H07-
42	241.6	33.1	863	5	BQ952037	BQ952037 AGENCOURT
43	239.4	32.8	623	4	BG964955	BG964955 602829272
44	239.4	32.8	958	5	BU523796	BU523796 AGENCOURT
45	239.4	32.8	1090	5	BQ960190	BQ960190 AGENCOURT

ALIGNMENTS

RESULT 1
CK629396/c
LOCUS CK629396 872 bp mRNA linear EST 26-MAR-2004
DEFINITION AM0-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA, mRNA sequence.
ACCESSION CK629396
VERSION CK629396.1 GI:45753871
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 872)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G., Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F., Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R., Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M., Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A. Jr.
TITLE Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
JOURNAL Unpublished (2004)
COMMENT Contact: Silva Jr, W. A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FMRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 39639300
Fax: +55 16 39639309
Email: wilsonjr@usp.br
This sequence was derived from the FAPESP Genome Program
High quality sequence start: 66
High quality sequence stop: 625.
FEATURES Location/Qualifiers
source 1. .872
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0013"
/note="Organ: whole body"
ORIGIN

Query Match 39.9%; Score 291; DB 7; Length 872;

```
  Best Local Similarity   68.3%;  Pred. No. 1.6e-76;
  Matches  446;  Conservative    1;  Mismatches  199;  Indels    7;  Gaps    3;

Qy         77 GTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTG 136
              | |||    |||||  | ||  | ||  |||||||| ||||  | || | ||  | ||||
Db        752 GCTACATCTTCACAAGTTATGATATAGACTGGGTGAGGCAGACGCCTGAACAGGGACTTG 693

Qy        137 AGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTCAAGG 196
              ||||||||||| |  ||  ||||     | ||    ||||  |||||  |||| |||||||
Db        692 AGTGGATTGGATGGTTTT-TCCTGGAGAGGGGAGTACTGAATACAATGAGAAGTTCAAGG 634

Qy        197 ACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGCAGCC 256
              || | ||| | | | ||||||||||||| |||| |||||||||  |||||||||   || |
Db        633 GCAGGCCCACACTGAGTGTAGACAAGTCCTCCAGCACAGCCTATATGGAGCTCACTAGGC 574

Qy        257 TGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAACTATG 316
              |||||||||||||||||| ||||||| |||||| |||           || |  |||
Db        573 TGACATCTGAGGACTCTGCTGTCTATTTCTGTGCTAGAGGGGACTACTATAGGCGCTACT 514

Qy        317 TTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGGAGCG 376
              ||   ||||  ||||  ||||  ||| | ||||||||||||||| |||| |  ||    |
Db        513 TT---GACTTGTGGGNCCAAGGGACCACGGTCACCGTCTCCTCATGTGGAGNCGGTTCAG 457

Qy        377 GTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACATTCC 436
              | || || ||| |||||| |||||||||   |||| | | |||||| |||| || ||
Db        456 GCGGAGGTGGCTCTGGCGGTGGCGGATCTGACATTGAGCTCACCCAGTCTCCAGCAATCA 397

Qy        437 TGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTA 496
              ||  ||  ||  |||| || ||||| |||| ||||||| |||||    ||| | ||
Db        396 TGTCTGCATCTCCAGGGGAGAGGGTCACCATGACCTGCAGTGCCAGCTCAAGTATACGTT 337

Qy        497 ATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATA 556
              |     || :|||||||||||||||||| ||    || || | ||| || || |   | |
Db        336 ACA---TATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTGATTTATGACA 280

Qy        557 CATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACGGATT 616
              ||||||         ||||||||||  |||||||| ||||||||| | ||||||   ||
Db        279 CATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTT 220

Qy        617 TCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAG 676
                || |||| |||| |    || |||||||| ||    ||   ||||| ||| ||| |
Db        219 ATTCTCTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTACTGCCAGGAGT 160

Qy        677 ATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGG 729
                  |  || |||    |||||||| || || ||||||||||  | ||||||
Db        159 GGAGTGGTTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGCTGAAACGG 107


RESULT 2
BQ474958/c
LOCUS       BQ474958                601 bp    mRNA    linear   EST 30-NOV-2002
DEFINITION  carabus4g12.b Carabus granulatus cDNA Carabus granulatus cDNA clone
            carabus4g12 5', mRNA sequence.
ACCESSION   BQ474958
VERSION     BQ474958.1  GI:25957232
KEYWORDS    EST.
SOURCE      Carabus granulatus
  ORGANISM  Carabus granulatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Coleoptera; Adephaga; Carabidae; Carabini;
            Carabina; Carabus; Carabus.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Theodorides,K., de Riva,A., Gomez-Zurita,J., Foster,P.G. and
            Vogler,A.P.
  TITLE     Comparison of EST libraries from seven beetle species: towards a
            framework for phylogenomics of the Coleoptera
  JOURNAL   Insect Mol. Biol. 11 (5), 467-475 (2003)
  MEDLINE   22217875
   PUBMED   12230545
COMMENT     Contact: Foster PG
            Vogler, Entomology
            The Natural History Museum
            Cromwell Road, London, SW7 5BD
            Email: p.foster@nhm.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Carabus granulatus"
                     /mol_type="mRNA"
                     /db_xref="taxon:118799"
                     /clone="carabus4g12"
                     /clone_lib="Carabus granulatus cDNA"
                     /note="Vector: pUC18"
ORIGIN

  Query Match           39.0%;  Score 284.4;  DB 5;  Length 601;
  Best Local Similarity   69.3%;  Pred. No. 1.4e-74;
  Matches  417;  Conservative    1;  Mismatches  178;  Indels    6;  Gaps    2;

Qy        128 AGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGA 187
              || | |||||||||||||| | |||  ||||     | ||   ||||  |||||  |||
Db        600 AGGGACTTGAGTGGATTGGATGGATTTTTCCTGGAGAGGGGAGTACTGAATACAATGAGA 541

Qy        188 AATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGC 247
              | ||||||| || ||||| | | | |||||||||||| |||| |||||||| |||||||
Db        540 AGTTCAAGGGCAGGGCCACACTGAGTGTAGACAAGTCCTCCAGCACAGCCTATATGGAGC 481

Qy        248 TCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTA 307
              ||   || ||||||||||||||||||| ||||||| |||||| |||           ||
Db        480 TCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTTCTGTGCTAGAGGGGACTACTATA 421

Qy        308 CGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTG 367
              |  |||  ||   ||||  ||||| |||| |||  | |||||||||||||| |||| |
Db        420 GGCGCTACTTT---GACTTGTGGGGCCAAGGGACCACGGTCACCGTCTCCTCATGTGGAG 364

Qy        368 GTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACTC 427
              | ||   || || || ||| ||||||| |||||||||    |||| | | |||||| |||
Db        363 GCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCTGACATTGAGCTCACCCAGTCTC 304

Qy        428 CCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGA 487
              |  || || ||  ||  ||  |||| || ||||| ||||| |||||||  |||||     |
Db        303 CAGCAATCATGTCTGCATCTCCAGGGGAGAGGGTCACCATGACCTGCAGTGCCAGCTCAA 244

Qy        488 GTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCA 547
              || |  |   | |  || :|||||||||||||||||| ||     || || | ||| || |
Db        243 GTATACG---TTACATATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTGA 187

Qy        548 TATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATG 607
              | |   | |||||||          ||||||||||  |||||||| ||||||||  | ||
Db        186 TTTATGACACATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCTG 127

Qy        608 GGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCT 667
              ||||   ||   || |||| |||| |   || ||||||| ||    ||   ||||| ||
Db        126 GGACCTCTTATTCTCTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTACT 67

Qy        668 GTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAAC 727
              | ||| |       |  || |||     |||||||| || || ||||||||||  | ||||
Db         66 GCCAGGAGTGGAGTGGTTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGCTGAAAC 7

Qy        728 GG 729
              ||
Db          6 GG 5


RESULT 3
CK629846/c
LOCUS       CK629846                1104 bp    mRNA    linear   EST 26-MAR-2004
DEFINITION  AM2-AA0023-091202-021-F02 AA0023 Apis mellifera cDNA, mRNA
            sequence.
ACCESSION   CK629846
VERSION     CK629846.1  GI:45754321
KEYWORDS    EST.
SOURCE      Apis mellifera (honey bee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
```

```
REFERENCE   1  (bases 1 to 1104)
  AUTHORS   Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
            Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
            Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
            Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
            Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,
            Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
            Silva,W.A. Jr.
  TITLE     Open reading frame ESTs - an efficient strategy for analysis of the
            honey bee transcriptome
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Silva Jr, W. A.
            Molecular Genetic and Bioinformatics Laboratory
            Departament of Genetics, FMRP/USP, FUNDHERP
            Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
            Tel: +55 16 39639300
            Fax: +55 16 39639309
            Email: wilsonjr@usp.br
            This sequence was derived from the FAPESP Genome Program
            High quality sequence start: 64
            High quality sequence stop: 594.
FEATURES             Location/Qualifiers
     source          1. .1104
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="Africanized"
                     /db_xref="taxon:7460"
                     /sex="female, worker"
                     /dev_stage="adult"
                     /clone_lib="AA0023"
                     /note="Organ: whole body"
ORIGIN

  Query Match           38.9%;  Score 283.4;  DB 7;  Length 1104;
  Best Local Similarity   68.2%;  Pred. No. 3.5e-74;
  Matches  452;  Conservative    1;  Mismatches  203;  Indels    7;  Gaps    4;

Qy         68 AGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGA- 126
              |||||||| | |||   |||||  | ||  | ||  |||||  ||| |||||  | || |
Db        747 AGGCTTCTTGCTACATCTTCACAAGTTATGATATAGACTGGTTGAGGCAGACGCCTGAAC 688

Qy        127 AAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAG 186
              ||| | ||||||||||||||| | |||  ||||    | ||   ||||   |||||  ||
Db        687 AAGGGACTTGAGTGGATTGGATGGATTTTTCCTGGAGAGGGGAGTACTGAATACAATGAG 628

Qy        187 AAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAG 246
              || ||||||| || | | | | | ||||||||||||| |||| |||||||||  ||||||
Db        627 AAGTTCAAGGGCAGGCCAACACTGAGTGTAGACAAGTCCTCCAGCACAGCCTATATGGAG 568

Qy        247 CTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATT 306
              |||   || |||||||||||||||||||| |||||||  ||||||  |||       | | |
Db        567 CTCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTTCTGTGCTAGA--GGGGACTACT 510

Qy        307 ACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGT 366
              |    |  | | ||   |  |||| ||||  |||  | ||||||||||||||| ||||
Db        509 ATAGGCGCTACTTTGACTTGTGGGGGCCAAGGGACCACGGTCACCGTCTCCTCATGTGGA 450

Qy        367 GGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCAGACT 426
              |  ||    || || || ||| ||||||| |||||||||   |||| | | ||||||  ||
Db        449 GACGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCTGACATTGAGCTCACCCAGTCT 390

Qy        427 CCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAG 486
              ||  || || ||  ||  ||  |||| || ||||| ||||| |||||||  |||||
Db        389 CCAGCAATCATGTCTGCATCTCCAGGGGAGAGGGTCACCATGACCTGCAGTGCCAGCTCA 330

Qy        487 AGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTC 546
              ||| |  |   | |  || :|||||||||||||||||| ||    || || | ||| ||
Db        329 AGTATACG---TTACATATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTG 273

Qy        547 ATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATAT 606
              || |   | |||||||          |||||||||||  |||||||| |||||||| | ||
Db        272 ATTTATGACACATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCT 213

Qy        607 GGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTC 666
              |||||   ||   || |||| |||| |    || ||||||| ||    ||   ||||| |
Db        212 GGGACCTCTTATTCTCTCACAATCAACCGAATGGAGGCTGAGGATGCTGCCACTTATTAC 153

Qy        667 TGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 726
              || ||| |      |  || |||    |||||||| || || ||||||||||  | |||
Db        152 TGCCAGGAGTGGAGTGGTTATCCGTACACGTTCGGAGG-GGGACCAAGCTGGAGCTGAAA 94

Qy        727 CGG 729
              |||
Db         93 CGG 91


RESULT 4
BQ921928
LOCUS       BQ921928               1010 bp    mRNA    linear   EST 20-AUG-2002
DEFINITION  AGENCOURT_8952829 NCI_CGAP_Co24 Mus musculus cDNA clone
            IMAGE:6475284 5', mRNA sequence.
ACCESSION   BQ921928
VERSION     BQ921928.1  GI:22336959
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1010)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14013  row: m  column: 13
            High quality sequence stop: 608.
FEATURES             Location/Qualifiers
     source          1. .1010
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6475284"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match           38.7%;  Score 282.4;  DB 5;  Length 1010;
  Best Local Similarity   87.9%;  Pred. No. 6.8e-74;
  Matches  320;  Conservative    0;  Mismatches   41;  Indels    3;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||| ||||||||||||||||  |||||||||||||||||||||||||||||||
Db         69 GAGGTCCAGCTGCAGCAGTCTGGACCTGAGATGGTGAAGCCTGGGGCTTCAGTGAAGATA 128

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||||||||||||| ||| |||||||| ||||||||||||||||||||||||||||||
Db        129 TCCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTGAAGCAGAGC 188

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||| |||||||||||||||||||| |||||||||  |||||||  | |   ||
Db        189 CATGGAAAGCGCCTTGAGTGGATTGGACGTGTTAATCCTAATAATGGTGAAAGTAGGTAT 248

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              |||||||| | | ||| |||||||| ||| |||||  |||||  || ||||||||||||||
```

```
Db        249 AACCAGAAGTCCGAGGGCAAGGCCACATTGACTGTTGACAAATCCTCCACCACAGCCTAC 308

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              |||||||||  |||||||||||||||||||||||||||||||| |||||||| | |||    |
Db        309 ATGGAGCTCAACAGCCTGACATCTGAGGACTCTGCGGTCTACTACTGTGCGATATCCTAT 368

Qy        301 ATGAT---TACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
              | |||         |||||| |||||||||||||||||||| ||||||||||||||||||
Db        369 AGGATCGGAGATTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 428

Qy        358 TCAG 361
              ||||
Db        429 TCAG 432


RESULT 5
BE309592
LOCUS       BE309592                 594 bp    mRNA    linear   EST 26-OCT-2000
DEFINITION  601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
            mRNA sequence.
ACCESSION   BE309592
VERSION     BE309592.1  GI:9168025
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8530  row: o  column: 12
            High quality sequence stop: 591.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="mix FVB/N, C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3489635"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam5"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
ORIGIN

  Query Match           38.5%;  Score 280.8;  DB 2;  Length 594;
  Best Local Similarity   91.7%;  Pred. No. 1.8e-73;
  Matches  297;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        406 AGTATTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACC 465
              | | |||||||||||||||||||| |||||||||||| ||||||||||||||||||||||
Db         47 AATGTTGTGATGACCCAGACTCCCAAATTCCTGCTTGTATCAGCAGGAGACAGGGTTACC 106

Qy        466 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCA 525
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        107 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCA 166

Qy        526 GGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGAT 585
              |||||||||||||| ||| || |||| |||| |||||| ||||||| ||||||||||||||
Db        167 GGGCAGTCTCCTAAACTTCTGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGAT 226

Qy        586 CGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCT 645
              ||||||| |||||||||||||||||||||||||||||||||||||||| |||| ||||||||
Db        227 CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCACCACTGTGCAGGCT 286

Qy        646 GAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGA 705
              |||||||||||| |||||||||||||||| |||||||  |||||    |||||||| ||
Db        287 GAAGACCTGGCATTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGG 346

Qy        706 GGCACCAAGCTGGAAATCAAACGG 729
              || |||||||||||||| ||||||
Db        347 GGGACCAAGCTGGAAATAAAACGG 370


RESULT 6
BF168514
LOCUS       BF168514                 724 bp    mRNA    linear   EST 30-OCT-2000
DEFINITION  601775412F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',
            mRNA sequence.
ACCESSION   BF168514
VERSION     BF168514.1  GI:11048866
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9265  row: h  column: 04
            High quality sequence stop: 661.
FEATURES             Location/Qualifiers
     source          1. .724
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4017075"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match           37.6%;  Score 273.8;  DB 2;  Length 724;
  Best Local Similarity   87.3%;  Pred. No. 2.5e-71;
  Matches  315;  Conservative    0;  Mismatches   37;  Indels    9;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||
Db         95 GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 154

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        155 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAAAGT 214

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
```

```
Db        215 CCTGAAAAGAGCCTTGAGTGGATTGGAGAGATTAATCCTAGCACTGGTGGTACTACCTAC 274

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Db        275 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC 334

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Db        335 ATGCAGCTCAAGAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA------ 388

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Db        389 ---AGCTACATCAGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 445

Qy        361 G 361

Db        446 G 446


RESULT 7
BF168856
LOCUS       BF168856                769 bp    mRNA    linear   EST 30-OCT-2000
DEFINITION  601775314F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017147 5',
            mRNA sequence.
ACCESSION   BF168856
VERSION     BF168856.1  GI:11049208
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9265  row: k  column: 04
            High quality sequence stop: 678.
FEATURES             Location/Qualifiers
     source          1. .769
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4017147"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match           37.3%;  Score 272.2;  DB 2;  Length 769;
  Best Local Similarity   87.0%;  Pred. No. 7.7e-71;
  Matches  314;  Conservative    0;  Mismatches   38;  Indels    9;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60

Db         99 GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 158

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120

Db        159 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAAAGT 218

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180

Db        219 CCTGAAAAGAGCCTTGAGTGGATTGGAGAGATTAATCCTAGCACTGGTGGTACTACCTAC 278

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240

Db        279 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC 338

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300

Db        339 ATGCAGCTCAAGAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA------ 392

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360

Db        393 ---AGCTACATCAGGGCTATGGACTACTGCGGTCAAGGAACCTCAGTCACCGTCTCCTCA 449

Qy        361 G 361

Db        450 G 450


RESULT 8
BF015548
LOCUS       BF015548                507 bp    mRNA    linear   EST 29-DEC-2000
DEFINITION  uy23a08.y1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3660374 5'
            similar to SW:HV14_MOUSE P01758 IG HEAVY CHAIN V REGION 108A
            PRECURSOR. ;, mRNA sequence.
ACCESSION   BF015548
VERSION     BF015548.1  GI:10746880
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

            MGI:1421142
            Seq primer: -40RP from Gibco
            High quality sequence stop: 456.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3660374"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu30"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: Oligo
                     dT.   Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match           37.0%;  Score 270;  DB 2;  Length 507;
```

```
  Best Local Similarity   85.5%;  Pred. No. 3.2e-70;
  Matches  313;  Conservative    0;  Mismatches   50;  Indels    3;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||| || ||||||||||||| ||||||||||||||||||||||||||||||||
Db         92 GAGGTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 151

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||
Db        152 TCCTGCAAGGCTTCTGGATACACATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 211

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              |||||||||||||||||||||||||| | ||||||||| |||||||| ||||  ||||
Db        212 CATGGAAAGAGCCTTGAGTGGATTGGACTTGTTAATCCTAGCAATGGTGATACTAGCTAC 271

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              |||||||| ||||||| |||||||| ||| |||||||||| || |||| |||||||||
Db        272 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC 331

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCT--- 297
              |||||||||  |||||||||||||||||||||| ||||||||||||||||||| |
Db        332 ATGGAGCTCAACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGATATTAC 391

Qy        298 ACTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
                |   ||  |||    | ||   ||||||   ||  ||| | ||||||||||||
Db        392 TACAGTGGTAGCTACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCC 451

Qy        358 TCAGGT 363
              ||||| |
Db        452 TCAGCT 457


RESULT 9
CK629415/c
LOCUS       CK629415               1419 bp    mRNA    linear   EST 26-MAR-2004
DEFINITION  AM1-AA0014-041102-021-H09 AA0014 Apis mellifera cDNA, mRNA
            sequence.
ACCESSION   CK629415
VERSION     CK629415.1  GI:45753890
KEYWORDS    EST.
SOURCE      Apis mellifera (honey bee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 1419)
  AUTHORS   Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G.,
            Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F.,
            Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R.,
            Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G.,
            Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,
            Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
            Silva,W.A. Jr.
  TITLE     Open reading frame ESTs - an efficient strategy for analysis of the
            honey bee transcriptome
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Silva Jr, W. A.
            Molecular Genetic and Bioinformatics Laboratory
            Departament of Genetics, FMRP/USP, FUNDHERP
            Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
            Tel: +55 16 39639300
            Fax: +55 16 39639309
            Email: wilsonjr@usp.br
            This sequence was derived from the FAPESP Genome Program
            High quality sequence start: 63
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
     source          1. .1419
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="Africanized"
                     /db_xref="taxon:7460"
                     /sex="female, worker"
                     /dev_stage="adult"
                     /clone_lib="AA0014"
                     /note="Organ: whole body"
ORIGIN

  Query Match            37.0%;  Score 269.4;  DB 7;  Length 1419;
  Best Local Similarity  68.8%;  Pred. No. 6.7e-70;
  Matches  427;  Conservative    1;  Mismatches  185;  Indels    8;  Gaps    4;

Qy        108 GGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGG 167
              |||||||||| | || | || | ||||||||||||||| | |||  ||||    | ||
Db        703 GGTGAAGCAGACGCCTGNACAG-GACTTGAGTGGATTGGATG-ATTTTTCCTGGAGAGGG 646

Qy        168 TGTTACTCTCTACAACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATC 227
                ||||   |||||  |||| ||||||| || |  || | | | ||||||||||||| ||
Db        645 ANGTACTGAATACAATGAGAAGTTCAAGGGCAGGCACACACTGAGTGTAGACAAGTCCTC 586

Qy        228 CACCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTG 287
              || ||||||||| |||||||||   || ||||||||||||||||||| ||||||| |||
Db        585 CAGCACAGCCTATATGGAGCTCACTAGGCTGACATCTGAGGACTCTGCTGTCTATTTCTG 526

Qy        288 TGCAAGATCTACTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGT 347
              ||| |||           || |  |||  ||   ||||  ||||| ||||  ||| | ||
Db        525 TGCTAGAGGGGACTACTATAGGCGCTACTTT---GACTTGTGGGGCCAAGGGACCACGGT 469

Qy        348 CACCGTCTCCTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAG 407
              |||||||||||| |||| |  ||     || || || ||| ||| ||| |||||||||
Db        468 CACCGTCTCCTCATGTGGAGACGGTTCAGGCGGAGGTGGCTCTGTCGGTGGCGGATCTGA 409

Qy        408 TATTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCAT 467
              |||| | | |||||| ||||  || || ||  ||  ||  |||| || ||||| |||||
Db        408 CATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGGTCACCAT 349

Qy        468 AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGG 527
              |||||||  |||||    ||| |  || |     || :|||||||||||||||||| ||
Db        348 GACCTGCAGTGCCAGCTCAAGTATACGTTACA---TATATTGGTACCAACAGAAGCCTGG 292

Qy        528 GCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCG 587
                || || | ||| || || |   | |||||||          |||||||||||  |||
Db        291 ATCCTCCCCCAGACTCCTGATTTATGACACATCCAACGTGGCTCCTGGAGTCCCTTTTCG 232

Qy        588 CTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGA 647
              ||||| |||||||| | ||||||   ||   || |||| |||| |    || |||||||
Db        231 CTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCAACCGAATGGAGGCTGA 172

Qy        648 AGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGG 707
              ||    ||  ||||| ||| ||| |      |  || |||    |||||||| || ||
Db        171 GGATGCTGCCACTTATTACTGCCAGGAGTGGAGTGCTTATCCGTACACGTTCGGAGGGGG 112

Qy        708 CACCAAGCTGGAAATCAAACG 728
              |||||||||||  | |||||
Db        111 GACCAAGCTGGAGCTGAAACG 91


RESULT 10
BF580610
LOCUS       BF580610               883 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5',
            mRNA sequence.
ACCESSION   BF580610
VERSION     BF580610.1  GI:11654322
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
```

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9771 row: l column: 07
High quality sequence stop: 639.

FEATURES Location/Qualifiers
source 1. .883
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4208022"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 36.8%; Score 268; DB 2; Length 883;
Best Local Similarity 93.2%; Pred. No. 1.5e-69;
Matches 302; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

```
Qy        406 AGTATTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACC 465
              | |||| |||||||||||||||||| |||||||| ||| ||||||||||||||||||||||
Db         72 ATTATTTTGATGACCCAGACTCCCAAATTCCTGC-TGTATCAGCAGGAGACAGGGTTACC 130

Qy        466 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCA 525
              |||||||||||||||||||||||||||||||||||||||  ||||||||||||||| ||
Db        131 ATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAG-CTGGTACCAACAGAAGTCA 189

Qy        526 GGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGAT 585
              |||||||||||||| |||||| |||| |||| |||||| ||||||  ||||||||||||||
Db        190 GGGCAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTATACTGGAGTCCCTGAT 249

Qy        586 CGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCT 645
              ||||||| |||||||||| |||||||||||||||||||||||||||||||| ||||||||
Db        250 CGCTTCACTGGCAGTGGACATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCT 309

Qy        646 GAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGA 705
              |||||||||||||||||||||||||||||| |||||||  ||||||| ||||||||||||||
Db        310 GAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCTCGGACGTTCGGTGGA 369

Qy        706 GGCACCAAGCTGGAAATCAAACGG 729
              |||||||||||||||||||||||||
Db        370 GGCACCAAGCTGGAAATCAAACGG 393
```

RESULT 11
BU523606
LOCUS BU523606 931 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10169250 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6530296 5', mRNA sequence.
ACCESSION BU523606
VERSION BU523606.1 GI:22834045
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14131 row: m column: 16
High quality sequence stop: 582.

FEATURES Location/Qualifiers
source 1. .931
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6530296"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 36.6%; Score 266.6; DB 5; Length 931;
Best Local Similarity 85.6%; Pred. No. 4.1e-69;
Matches 309; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

```
Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||||  || ||  |||||||||||  |||||||||||||||||||||||||||||
Db         97 GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATG 156

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||  |||||||||||  |||  ||  ||||||  ||||||||||  ||||||||||||||||
Db        157 TCCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGAACTGGGTGAAGCAGAGC 216

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||  ||||||||||||||||  |||||||||  ||||  ||||  ||||  ||
Db        217 CATGGAAAGACCCTTGAGTGGATTGGAGATATTAATCCTTACAACGGTGGTACTAGCTTT 276

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              ||||||||  ||||||||||||||||  |||  ||||||||||  |  ||||  |||||||  |
Db        277 AACCAGAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAACCCTCCAGGACAGCCTTC 336

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              |||  |  |||   ||||||||||||||||||||||||  ||||||||  ||||||||||
Db        337 ATGCACCTCAATAGCCTGACATCTGAGGACTCTGCAGTCTATTATTGTGCAAGATCGGGC 396

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                 |  |   |||||  ||||||||||||||||||||  ||||||||||||||||||||||
Db        397 TATGATTC---CTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 453

Qy        361 G 361
              |
Db        454 G 454
```

RESULT 12
CK629414/c
LOCUS CK629414 1339 bp mRNA linear EST 26-MAR-2004
DEFINITION AM1-AA0014-041102-021-D05 AA0014 Apis mellifera cDNA, mRNA sequence.
ACCESSION CK629414
VERSION CK629414.1 GI:45753889
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 1339)
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G., Maia,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F., Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R., Ramos,R.G.P., Reis,L.F.L, Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zago,M.A., Soares,A.E.E., Bitondi,M.M.G., Espreafico,E.M.,

```
            Espindola,F.S., Paco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and
            Silva,W.A. Jr.
  TITLE     Open reading frame ESTs - an efficient strategy for analysis of the
            honey bee transcriptome
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Silva Jr, W. A.
            Molecular Genetic and Bioinformatics Laboratory
            Departament of Genetics, FMRP/USP, FUNDHERP
            Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
            Tel: +55 16 39639300
            Fax: +55 16 39639309
            Email: wilsonjr@usp.br
            This sequence was derived from the FAPESP Genome Program
            High quality sequence start: 62
            High quality sequence stop: 662.
FEATURES             Location/Qualifiers
     source          1. .1339
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="Africanized"
                     /db_xref="taxon:7460"
                     /sex="female, worker"
                     /dev_stage="adult"
                     /clone_lib="AA0014"
                     /note="Organ: whole body"
ORIGIN

  Query Match           36.3%;  Score 264.4;  DB 7;  Length 1339;
  Best Local Similarity   67.6%;  Pred. No. 2.1e-68;
  Matches  431;  Conservative    1;  Mismatches  198;  Indels    8;  Gaps    4;

Qy         94 TACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGG-ACGTAT 152
              ||  | ||   || |||||     |  | || | ||  ||||||||||| ||| |   ||
Db        721 TATGATATAGCCTCGGTGAGCAGAACGCCTGAACAGGACCTTGAGTGGACTGGAATCGAT 662

Qy        153 TAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTCAAGGACAAGGCCATATTAAC 212
              |  ||||    | ||. ||||   |||||  |||| |||||| || ||||| | | |
Db        661 TTTTCCTGGAGAGGGGAGTACTGAATACAATGAGAAGTTCAAGGGCAGGGCCACACTGAG 602

Qy        213 T-GTAGACAAGTCATCCACCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACT 271
              | |||||||||| |||| |||||||||| |||||||||    || ||||||||||||||
Db        601 TGGTAGACAAGTCCTCCAGCACAGCCTATATGGAGCTCACTAGGCTGACATCTGAGGACT 542

Qy        272 CTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAACTATGTTATGGACTACTGGG 331
              |||| ||||||| |||||| |||           || |  |||  ||   |||| ||||
Db        541 CTGCTGTCTATTTCTGTGCTAGAGGGGACTACTATAGGCGCTACTTT---GACTTGTGGG 485

Qy        332 GTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGTGGTGGGAGCGGTGGTGGCGGCACTG 391
              ||||  ||| | ||||||||||||||| |||| || ||    || || || ||| |||
Db        484 TCCAAGGGACCACGGTCACCGTCTCCTCATGTGGAGGCGGTTCAGGCGGAGGTGGCTCTG 425

Qy        392 GCGGCGGCGGATCTAGTATTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAG 451
              |||| |||||||||    |||| | | |||||| |||| || || ||  ||  || |||
Db        424 GCGGTGGCGGATCTGACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAG 365

Qy        452 GAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGT 511
              | || ||||| ||||| ||||||| |||||     ||| |  || |      || :|||||
Db        364 GGGAGAGGGTCACCATGACCTGCAGTGCCAGCTCAAGTATACGTTACA---TATATTGGT 308

Qy        512 ACCAACAGAAGCCAGGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACG 571
              |||||||||||| ||    || || | ||| || || |   | |||||||
Db        307 ACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTGATTTATGACACATCCAACGTGGCTC 248

Qy        572 CTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCA 631
              ||||||||||  |||||||| |||||||| | ||||||   ||   || |||| ||||
Db        247 CTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTATTCTCTCACAATCA 188

Qy        632 GCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTC 691
              |    || |||||||  ||    ||   ||||| ||| ||| |       |  || |||
Db        187 ACCGAATGGAGGCTGAGGATGCTGCCACTTATTACTGCCAGGAGTGGAGTGGTTATCCGT 128

Qy        692 CGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGG 729
              |||||||| || || ||||||||||  | ||||||
```

```
Db        127 ACACGTTCGGAGGGGGGACCAAGCTGGAGCTGAAACGG 90


RESULT 13
BI104341
LOCUS       BI104341                598 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602889919F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035013 5',
            mRNA sequence.
ACCESSION   BI104341
VERSION     BI104341.1  GI:14555234
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11097  row: f  column: 06
            High quality sequence stop: 598.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5035013"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu29"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match           36.2%;  Score 263.6;  DB 4;  Length 598;
  Best Local Similarity   84.3%;  Pred. No. 2.9e-68;
  Matches  312;  Conservative    0;  Mismatches   49;  Indels    9;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||| || |||||||| |||| ||||||||||||||||||||||||||||||
Db         92 GAGGTCCAGCTGCAACAGTCTGGAGCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 151

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||||||||||||| ||| |||||| || |||| ||||| ||||||||||||||||||
Db        152 TCCTGCAAGGCTTCTGGCTACACATTCAATGACTACAACATGGACTGGGTGAAGCAGAGC 211

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              |||||||||||||||||||||||||  |||||||||||| ||| |  |||| |||||
Db        212 CATGGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTAACTATGATAGTACTATCTAC 271

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              |||||||| ||||||| |||||||| ||| |||||||| ||||| |||| ||||||||||
Db        272 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGAGAAGTCCTCCAGCACAGCCTAC 331

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||  |
Db        332 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGATCGATG 391

Qy        301 ATGATTACG---------AACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACC 351
                 | |   |           |||     | |||||||||| ||||  ||| |  ||||
```

```
Db        392 GGGTTACGGGGGTGGGGCCCCTACTACTTTGACTACTGGGGCCAAGGCACCACTATCACA 451

Qy        352 GTCTCCTCAG 361
              ||||||||||
Db        452 GTCTCCTCAG 461


RESULT 14
BX969451
LOCUS       BX969451                842 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Reverse strand read from insert in 5'HPRT insertion targeting and
            chromosome engineering clone MHPN79o16, genomic survey sequence.
ACCESSION   BX969451
VERSION     BX969451.1  GI:49700874
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 842)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .842
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPN79o16"
                     /clone_lib="MHPN"

ORIGIN

  Query Match            35.9%;  Score 262;  DB 9;  Length 842;
  Best Local Similarity  93.2%;  Pred. No. 9.9e-68;
  Matches  274;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              ||||| ||||| ||||||||| ||||||| |||||||||||||||||||||||||||||||
Db        284 GAGGTTCAGCTGCAGCAGTCTAGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 343

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 403

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              ||||||||||||||||||||||||||  |||| ||||| |||||||| || ||  ||||
Db        404 CATGGAAAGAGCCTTGAGTGGATTGGATATATTTATCCTTACAATGGTTTTTCTAGCTAC 463

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              |||||||| ||||||| |||||||| ||| |||||||||||||| || | ||||||||||
Db        464 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCTAGCACAGCCTAC 523

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        524 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA 577


RESULT 15
BF577847
LOCUS       BF577847                684 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602092155F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206540 5',
            mRNA sequence.
ACCESSION   BF577847
VERSION     BF577847.1  GI:11651559
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9767  row: n  column: 13
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4206540"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Co24"
                     /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.6 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            35.8%;  Score 261;  DB 2;  Length 684;
  Best Local Similarity  85.0%;  Pred. No. 1.9e-67;
  Matches  307;  Conservative    0;  Mismatches   45;  Indels    9;  Gaps    1;

Qy          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
              |||||||||||| || ||||||||||||| |||||||||||||||||||||||||||||||
Db         55 GAGGTCCAGCTGCACCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGATG 114

Qy         61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
              |||||||||||||||| ||| ||||||||  |||||||| |||||||||| ||| ||
Db        115 TCCTGCAAGGCTTCTGGATACACATTCACTAACTACTACATTCACTGGGTGAAACAGGGC 174

Qy        121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
              |||||||||||||||||||||||||||||  |||| |||||| ||||||||  |||   |||
Db        175 CATGGAAAGAGCCTTGAGTGGATTGGATATATTTATCCTAGCAATGGTGAGACTGGTTAC 234

Qy        181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
              |||||||| ||||||| |||||||| ||| |||||||||||||| |||| ||||||||||
Db        235 AACCAGAACTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTAC 294

Qy        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
              ||||| |||||||||||||||||||| || ||||| ||||||||||||||||||     |
Db        295 ATGGACCTCCGCAGCCTGACATCTGAAGATTCTGCAGTCTATTACTGTGCAAGAGACTTT 354

Qy        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                |         |      |||||||||||||||||| ||||||||||||||||||||
Db        355 GGTA---------ACTACGGGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 405

Qy        361 G 361
              |
Db        406 G 406


Search completed: March 14, 2005, 22:52:11
Job time : 3227 secs
```